erd 01/18/20

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 19, 2002, 16:32:27; search time 53.19 Seconds (without alignments) 682.856 Million cell updates/sec

Title: us-09-771-961-2 1709

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62 Sequence: Perfect score: 1 MCSTSGCDLEEIPLDDDDLN......WIQQHGGWEKILGISHEEVD 327

shed: 747574 segs, 111073796 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

					Database :
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:* 19: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:* 20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:* 21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* 22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*	14: /SIDSI/gcgdata/hold-genese4/geneseqp-embl/AA1994.DAT:* 15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:* 16: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:* 17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:* 17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*	10: /SIDS1/gcgdata/hold-genesed/genesedp-emb1/AA1990.DAT:* 11: /SIDS1/gcgdata/hold-genesed/genesedp-emb1/AA1991.DAT:* 12: /SIDS1/gcgdata/hold-genesed/genesedp-emb1/AA1992.DAT:* 13: /SIDS1/gcgdata/hold-genesedy-genesedp-emb1/AA1993.DAT:*	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:* 7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:* 8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:* 9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*	<ol> <li>/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*</li> <li>/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*</li> <li>/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*</li> <li>/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*</li> </ol>	A_Geneseq_032802:* 1: /SIDS1/9c9data/hold-geneseq/geneseqp-emb1/AA1980.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

10 11 11	765	2 w 4	1	Result No.
686 686 686 686 686	929.5 691.5	1709 1189.5 1189.5	1709	Score
40.1 40.1 40.1 40.1	40.5 40.1	69.6	100.0	Query Match Le
129 129 129	151 129	252	327	h Length DB
222	222	222	22	B ID
ABB18598 AAM53929 AAM66317	AAM95378 ABB27961 ABB33133	AAE07041 AAB85167	AAE07040	0
Protein #39/ Encor Human brain expres Human bone marrow	Human reproductive Human peptide #612 Peptide #639 encod	Human BCL-X-like P Human Bcl-Gs polype Mouse Bcl-G polype	Human BCL-X-11ke P Human Bcl-Gl Polyp	Description

1113 115 115 116 117 117 117 117 117 117 117 117 117
686 686 686 608 122.5 120 119.5 118.5 118.1 117 117 117 117 117 117 117 117 117 1
34.44 400.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11 700.11
129 129 178 4417 4411 190 225 249 233 233 233 233 233 233 233 233 233 23
222 222 222 222 222 222 221 14 21 17 21 17 22 22 22 22 22 22 22 22 22 22 22 22 22
AAM14186 AAM26596 AAM01922 ABG26266 AAU00222 AAW19396 AAU00219 AAR68884 AAW7393358 AAW7393358 AAW68887 AAW31530 AAR68887 AAW31530 AAW83123 AAW69969 AAW483122 AAW62962 AAW83122 AAW64262 AAW550538 AAW483122 AAW64262
peptide #620 encod peptide #604 encod Novel human diagno LFM Portos "Deprenyl" (RTM)-i BCl-X1-DTR apoptos Chicken lymphold B Apoptosis associat Rat wild-type BCl-X BCl-X protein. Human anti-apoptot BCl-X polypeptide. Human BCl-XL prote Human BCl-XL prote Human BCl-XL prote Protein encoded by Mouse BCL-X gamma. Mutant bcl-XL prote Human Dcl-XL prote Human Dcl-XL prote Human brain expres Human bone marrow peptide #9551 enco Protein #7655 enco Human bone marrow peptide #9884 enco Human BCl-XL (tran Arabidopsis thalia

ALIGNMENTS

RESULT NAE07040 \_

AAE07040 standard; Protein; 327 AA.

AAE07040;

23-OCT-2001 (first entry)

Human BCL-X-like protein #1.

Human; BCL-X-like protein; therapy; physiological disorder.

Homo sapiens.

WO200157213-A2.

31-JAN-2001; 2001WO-US03446.

09-AUG-2001 L

04-FEB-2000; 2000US-0180412.

(LEXI-) LEXICON GENETICS INC.

Donoho G, Sands AT; Hilbun E, Turner CA, Friedrich G, Abuin A, Zambrowicz B;

WPI; 2001-488882/53. N-PSDB; AAD13235.

Novel isolated human BCL-x-like polynucleotide, useful in therapeutic, diagnostic and pharmacogenic applications :

Claim 4; Page 30-31; 33pp; English.

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AAB85166
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        WPI; 2001-398125/42.
N-PSDB; AAH22582
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                                                               (BURN-) BURNHAM INST
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                                                                                                                                               21-JUN-2001.
                                                                                                                                                                                                         Bcl-G; cancer; cancer therapy; oncogene; apoptosis; Bcl-Gl; cytostatic;
antiapoptotic; chromosome 12p12.3; human.
                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                           Human Bcl-Gl polypeptide.
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                                                                                                                                                                                                                                                                                                                                      AAB85166 standard; Protein; 327 AA.
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The BCL-X-like polynucleotides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations treating the normal function of protein in the body and also for treating physiological disorders and diseases. The BCL-X-like polynucleotides are useful in conjunction with polymerase chain and sequencing templates and as hybridisation probes for assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LSYSVEKTITDOVLMGVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGEGTKY 300
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                                      09-AUG-2001.
                                                                                                      Human; BCL-X-like protein; therapy; physiological disorder.
                                                                 WO200157213-A2
                                                                                           Homo sapiens.
                                                                                                                                           Human BCL-X-like protein #2.
                                                                                                                                                                         23-OCT-2001 (first entry)
                                                                                                                                                                                                              AAE07041;
                                                                                                                                                                                                                             AAE07041 standard; Protein; 252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Bcl-G polypeptides and nucleic acids encoding them. The Bcl-G polypeptides can be expressed by standard recombinant specific antibodies are useful for diagnosing cancer, monitoring cancer polypeptides are useful for diagnosing cancer. The Bcl-G polypeptide. They are useful for identifying modulators, for modulating the activity of an oncogenic a level of apoptosis mediated by the Bcl-G polypeptide. A therapeutic composition comprising the Bcl-G polypeptide, Polypeptide of treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a human Bcl-Gl polypeptide.
                                                                                                                                                                                                                                                                                               301 lkenfspwigqhggwekilgisheevd 327
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04-FEB-2000; 2000US-0180412

(LEXI-) LEXICON GENETICS INC

Donoho G,

Hilbun E,

Turner CA,

Friedrich G,

Abuin A,

Zambrowicz B;

N-PSDB; AAD13236

WPI; 2001-488882/53.

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Claim 5; Page 32; 33pp; English.

Novel isolated human BCL-X-like polynucleotide, useful in therapeutic, diagnostic and pharmacogenic applications  $\dot{\phantom{a}}$ 

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gene expression patterns.

Sequence

252 AA;

The present sequence is human BCL-X-like protein.

The BCL-X-like polynucleotides are useful in therapeutic, diagnostic rate BCL-X-like polynucleotides. They are useful for screening drugs and pharmacogenic applications. They are useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations affective in the normal function of protein in the body and also for perturbing the normal function of protein in the BCL-X-like reacting physiological disorders and diseases. The BCL-X-like polynucleotides are useful in conjunction with polymerase chain polynucleotides are useful in conjunction with polymerase cloning reaction to screen libraries, isolate clones, to prepare cloning and sequencing templates and as hybridisation probes for assessing

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Query Match Best Local S

Local Similarity

69.68;

Score 1189.5; DB 22; Length 252; pred. No. 6.4e-113; 2; Mismatches 7; Indels 7;

7; Gaps

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232; Conservative

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121 EYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAETVYSWPPPQATQAGGFKSKEI 180

eyqdshsqqwsrclsnveqcleheavdpkvisianrvaelvyswpppqatqaggfkskei 180 FYTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKLKK------DKAL 233

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61 CSANESWTEVSWPCRNSOSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTL 120

1 MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGN 60

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В

241 qgfpqdgl 248

234 MGHFQDGL 241

AAB85167 standard; protein; 252 AA.

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AAB85167;

07-SEP-2001

(first entry)

RRESULT
AAB85167
ID AAB8
XX AAB8
AC AAB8
XC O7-4
XC O7-4
XX O7-4
XX BC1
KW BC1
KW ant
XX BC1
KW ant
XX HOM

antiapoptotic; Bcl-G; cancer;

WO200144282-A2. Homo sapiens.

21-JUN-2001

13-DEC-2000; 2000WO-US33793.

Human Bcl-Gs polypeptide.

cancer therapy; oncogene; apoptosis; Bcl-Gs; cytostatic; chromosome 12p12.3; human.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to Bcl-G polypeptides and nucleic acids encoding them. The Bcl-G polypeptides can be expressed by standard recombinant methodology. Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-G specific antibodies are useful for diagnosing cancer. The Bcl-G second for modulating the activity of an oncogenic therapy or assessing prognosis of patients with cancer. The Bcl-G polypeptides are useful for modulating the activity of an oncogenic the second for the second for identifying modulators, for modulating polypeptide. They are useful for identifying modulators, for modulating polypeptide. They are useful for identifying modulators, a therapeutic polypeptide. They are mediated by the Bcl-G polypeptide, a therapeutic alevel of apoptosis mediated by the Bcl-G polypeptide, polynucleotide or antibody a second for treating a pathology characterized by abnormal cell is useful for treating a pathology characterized by abnormal cell approliferation especially cancer. The present sequence represents a proliferation especially cancer.
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                                                                                                                                                                                                             AAB85188 standard; Protein; 328 AA.
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                                                                           Bcl-G; cancer; cancer therapy; oncogene; apoptosis; cytostatic; antiapoptotic; chromosome 12p12.3; mouse.
                                                                                                                       Mouse Bcl-G polypeptide.
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                                                                                                                                                           (first entry)
                          Location/Qualifiers
/label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.6%; Score 1189.5; DB 22; Length 252; 93.5%; Pred. No. 6.4e-113; pred. No. 6.4e-113; pred. No. 6.4e-113; pred. 7;
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AAM95378;
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                                                             AAM95378 standard; Protein; 151 AA.
                                                                                                                          292 RVIGEGTKYLKENESPWIQQHGGWEKILGISHEEVD 327
                                                                                                              293 rmlgfgtkylkeyfspwyggnggwekilgisheevd 328
                                                                                                                                                  233 almssfqdglsystfktitdlflrdvdtrgesevkargfkaalaidaiakitasdnhpmn
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                                                                                                                                                                                          176 areeasskrgsrrflyfrfeg---pwdsknkdgedqiiskivellkssgdqlgreikkdk 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Bcl-G polypeptides and nucleic acids encoding methodology. Bcl-G oligonucleotides (or its anti-sense strandard recombinant therapy or assessing prognosis of patients with cancer, monitoring cancer polypeptides are useful for identifying the activity of an oncogenic composition comprising the Bcl-G polypeptide. They are useful for identifying modulators, for modulating the activity of an oncogenic composition comprising the Bcl-G polypeptide. A therapeutic is useful for treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a
                                                                                                                                                                                                                                      120 pfpvergsgfhnqhwprsissveqpwrvklwipkwlvlptewlklf----tpghhqmsst 175
                                                                                                                                                                                                                                                          119 --TLEYODS-HSQOWSRCLSNYEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                               6
                                                                                                                                                                                                                                                                               61 ws-tdswtqvs1pcrgspsseknis1gkkksswrt1frvaekeeg1pxspkeiraggpqg 119
                                                                                                                                                                                                                                                                                                     61 CSANESWTEVSWPCRNSOSSEKAINLGKKKSSWKAFFGVVEKEDS-QSTPAKVSAQGQR- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Page 114-115; 117pp; English.
                                                                                                                                                                                                                                                                                                                           1 mcstsvydledipledddpnsiefkilafyarhhvfkntpavfspklsrtrsisgkalgt 60
                                                                                                                                                                                                                                                                                                                                       1 MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSORGLGN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotide encoding Bcl-G polypeptide, useful for modulating apoptosis, and for diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-398125/42.
N-PSDB; AAH22670.
                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-1999;
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Similarity 59.5%; Score 929.5; DB 22; Length 328;
00; Conservative 36; Mismatches 83; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                              328 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded by NGC"
                                                                                                                                                                                                                                                                                                                                                                    83; Indels 17; Gaps
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                                                                       08-SEP-2000;
12-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human reproductive system related antigen SEQ ID NO: 4036.
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2000US-0232081
2000US-0231968
2000US-0232397
2000US-0232398
2000US-0232398
2000US-0232400
2000US-0232400
2000US-0232400
2000US-0232400
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2000US-0225214
2000US-022526
2000US-022526
2000US-022528
2000US-022527
2000US-022527
2000US-022527
2000US-0225447
2000US-0225757
2000US-0225758
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2000US-0227182.
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2000US-0220963
2000US-0220964
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2000US-0190076.
2000US-0198123.
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AAM95378 RESULT

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26-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

2000US-0233064 2000US-0234223 2000US-0234274 2000US-0234297 2000US-0234997 2000US-023498 2000US-0235834 2000US-0235834 2000US-0235834 2000US-0235834 2000US-0235836

27-SEP-2000;

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08-DEC-2000; 2000US-0251999.

08-DEC-2000; 2000US-0251990.

11-DEC-2000; 2000US-0254097.

11-DEC-2001; 2000US-0259678.
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RESULT
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                                                                                                                                                                                                                                                                                                              ABB27961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used number of human reproductive system related system disorders, in the prevention and treatment of reproductive system disorders in the prevention and treatment of a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 4036; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              10 mcstsgcdleeiplddddintiefkilayytrhnyfkstpalfspkllrtrslsgrglgn 69
                   04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

26-MAY-2000; 2000US-0608408.

30-JUN-2000; 2000US-0632366.

03-AUG-2000; 2000US-0234687.

21-SEP-2000; 2000US-0236359.

27-SEP-2000; 2000US-0236359.

04-0CT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                   ABB27961 standard; Peptide; 129 AA.
                                                                                                                                                                                                                                                                                                                                                         130 eyqdshsss-gqvlsnveqvl 149
                                                                                                                                                                                                                                                                                                                                                                             121 EYODSHSOQWSRCLSNVEQCL 141
                                                                                                                                                                                                                                                                                                                                                                                                                         61 CSANESWIEVSWPCRNSOSSEKAINLGKKKSSWKAFFGVVEKEDSOSTPAKVSAGGORTI 120
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                                                                                                                                                                                                                                                         01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                               ABB27961;
                                                                                                                                                                                                 Human; microarray; single exon probe; gene expression; breast; disease; cancer.
                                                                                                                                                                                                                                 Human peptide #612 encoded by breast cell single exon nucleic acid probe-
                                                                                                                                                        WO200157271-A2
                                                                                                                                                                             Homo sapiens.
                                                                                                                                   09-AUG-2001.
                                                                                                           30-JAN-2001; 2001WO-US00662.
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(MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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; pred. No. 2.2e-62;
; pred. No. 5;
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08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246523.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246610.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0249207.
17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249214.

20-0CT-2000; 2000US-0241809; 20-0CT-2000; 2000US-0241829; 20-0CT-2000; 2000US-0244617; 01-NOV-2000; 2000US-0246474; 08-NOV-2000; 2000US-0246474; 08-NOV-2000; 2000US-0246475; 08-NOV-2000; 2000US-0246475; 2000US-0246476; 200

02-OCT-2000; 02-OCT-2000; 13-OCT-2000; 13-OCT-2000;

2000US-0236368 2000US-0236369 2000US-0236802 2000US-0237037 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0239935 2000US-0239935 2000US-0239936 2000US-0239937 2000US-0239937 2000US-0239937 2000US-0239937 2000US-0239937 2000US-0239937 2000US-0239937 2000US-0239937 2000US-0239937

2000US-0249245. 2000US-0249264. 2000US-0249265. 2000US-0249297. 2000US-0249299. 2000US-0249300.

2000US-0251479. 2000US-0251856. 2000US-0251868. 2000US-0251988. 2000US-0256719. 2000US-0256719. 2000US-0250160. 2000US-0250391.

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04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids contact the probes with a collection of detectably labelled nucleic acids contact ing the expression of human breast, and then measuring the label coverifying the expression of regions of genomic DNA predicted to expression predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of the microarray of this invention presents a far greater rapid production of functional information presents a far greater corpose of the invention. Information from genomic sequence tag microarrays. The method is suitable for probe of the invention. Information from genomic sequence. The corpose of the invention, but was obtained in electronic format directly in the contact of the contact of the invention, but was obtained in electronic format directly.
                                          30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                      WO200157277-A2.
                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                      Peptide #639 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                   04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                     121 nveqclehe 129
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                                                                                                                                                                                                                                                                                                                                                       61 nsqssekainlgkkksswkaffgvvekedsqstpakvsaqgqrtleyqdshsqqwsrcls 120
                                                                                                                                                                                                                                                                                                                                                                    76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
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                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 40.1%; Score 686; DB 22; Conservative 0; Mismatches 0;
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24-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
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                                                                                                                                                                                                                                                                                                         Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                       Protein #597 encoded by probe for measuring heart cell gene expression.
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03-AUG-2000; 2000US-053236.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234587.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.1%; Score 686; DB 22; Length 129; 100.0%; Pred. No. 6.3e-62; tive 0; Mismatches 0; Indels
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes for see the present invention relates to single exon nucleic acid probes for second probes in the present sequence is a protein encoded by one such a probe. The probes may be used for predicting, measuring and displaying probe. The probes may be used for predicting, measuring and incroarrays. ABA21335-ABA21369, the probes are useful for predicting, the probes are useful for predicting, the probes are useful for predicting, the gene expression, the probes are useful for predicting, the gene gene assuring gene expression, the probes are useful for predicting, the gene gene assuring gene expression, the probes are useful for predicting, the gene gene gene assuring gene expression, the probes are useful for predicting and prognosing disease. It is a probable of the printed diagnosing, and prognosing disease. It is a probable of the printed human heart and confident form part of the printed human heart sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from wife form and introduction in the probable of the printed and prognosing disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           penn SG,
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at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                    136 NVEQCLEHE 144
                                                                                                                                                                                                                                                                                                                              AAM53929 standard; protein; 129
                                                                                                                                                                                                                                                                                                                                                                                                      121 nveqclehe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                 AAM53929;
                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 26034.
                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; Human; brain expressed exon; gene expression analysis; probe; multiple sclerosis; schizophrenia; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                             epilepsy; cancer.
                                                                                                                                                  Homo sapiens.
                                                                                                                     WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                               10
04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
                                                                                           09-AUG-2001
                                                          30-JAN-2001; 2001WO-US00667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.1%; Score 686;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 129;
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21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
27-SEP-2000; 2000GB-0024263
04-OCT-2000; 2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which are derived from genomic sequences expression in brain cell samples, prain. They can be used to measure gene expression in of nervous system brain. They enable the diagnosis and improved treatment of nervous system which may enable the diagnosis and improved treatment of schizophrenia, which may enable the diagnosis and improved treatment is schizophrenia, brain and cancers. The present sequence is a protein encoded by one of epilepsy and cancers. The present sequence is a protein encoded by the epilepsy and cancers.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 DDDLNTIEEKILAYYTRHHYFKSTPALFSPKLLRTRSLSORGLGNCSANESWTEYSWPCR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 NSOSSEKAINLGKKKSSWKAFFGYVEKEDSOSTPAKVSAQGORTLEYQDSHSQQWSRCLS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed probe encoded protein SEQ ID NO: 26623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    дам66317;
                                                                                                                                                                                                                                                                                                                                                                      Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                         WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                             09-AUG-2001.
                                              21-SEP-2000;
27-SEP-2000.
                                                                                                                                     04-FEB-2000;
26-MAY-2000;
                                                                                                                30-JUN-2000;
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                                                                                              03-AUG-2000;
                         04-OCT-2000;
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                                   2000US-0608408
2000US-0608408
2000US-0632366
2000US-0234687
2000US-023687
2000US-0236359
2000US-024263
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                                                                                                                                                                      2000US-0180312.
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100.0%; Pred. No. 6.3e-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0207456; 30-JUN-2000; 2000US-069408; 21-SEP-2000; 2000US-0523667; 27-SEP-2000; 2000US-023687; 04-OCT-2000; 2000US-0236359; 04-OCT-2000; 2000US-0024263; 04-OCT-2000US-0024263; 04-OCT-2000; 2000US-0024263; 04-OCT-2000; 04-OCT-2000US-0024263; 04-OCT-2000; 04-OCT-20
WPI; 2001-488901/53.
                                                           Penn SG,
                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157278-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #620 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM14186 standard; Protein; 129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 nsqssekainlgkkksswkaffgvvekedsqstpakvsaqgqrtleyqdshsqqwsrcis 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 NSQSSEKAINLGKKKSSWKAFEGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human samples, which may can be used to measure gene expressed in the human such as lymphoma, Leukaemia and myeloma. The present seatment of cancers protein encoded by one of the probes of the invention.
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                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
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                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.18; Sc. No. 100.08; Pred. No. No. Mismatches
                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 686; DB 22;
Pred. No. 6.3e-62;
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04-FEB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456,
03-AUG-2000; 2000US-0608408
21-SED-2000; 2000US-052366,
27-SED-2000; 2000US-05234687,
27-SED-2000; 2000US-023659,
Human genome-derived single exon nucleic acid probes useful for
                                               WPI; 2001-488897/53.
                                                                         Penn SG,
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                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                         WO200157272-A2.
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                               Peptide #633 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                              17-0CT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 AAM26596 standard; Protein; 129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSOSTPAKVSAOGORTLEYODSHSOOWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human single exon nucleic acid probes by one such probe. The SENES are derived from human HeLa cells. The senesuring human gene expression in a sample derived from human HeLa cells. The SENES to epithelial cells. By measuring gene expression, the probes are the senestion and cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 DDDINTIEBKILAYYTRHHVFKSTPALESPKLLRTRSLSORGLGNCSANESWTEVSWPCR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 dddintiefkilayytrhhvfkstpalfspklirtrslsgrglgncsaneswtevswpcr 60
                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID No 19012; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                         2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100.
29; Conservative
                                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.1%; Score 686; DB 22; Length 12 100.0%; Pred. No. 6.3e-62; Length 12 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 129;
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analyzing gene expression in human placenta

Claim 27; SEQ ID NO 26865; 654pp; English.

The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from wipo at figure in the printed specification in the problem of the printed specification, but was obtained in electronic format directly from wipo specification in the problem of the printed specification in the problem of the problem of the printed specification in the problem of the prob
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     sequence 129 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #26257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                 Drmanac RT,
                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations diagnostics for genetic disorders or other traits and to assess responsible for genetic disorders or other traits.
                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers,
                                                                                                Claim 20; SEQ ID No 56625; 103pp; English.
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100.0%; Pred. No. 6.3e-62;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              Tang YT;
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RESULT 14 AAM01922

AAM01922;

AAM01922 standard; Protein; 129 AA.

WO200157270-A2 Homo sapiens.

09-AUG-2001.

29-JAN-2001; 2001WO-US00661.

Peptide #604 encoded by probe for measuring human breast gene expression.

inflammatory disease; proliferative breast disease; non-carcinoma tumour. probe; human; breast disease; breast cancer; development disorder;

Penn SG,

Hanzel DK,

Chen W,

Rank DR;

WPI; 2001-476286/51.

in a human breast

The present invention relates to novel single exon nucleic acid probes (see AAI100010-AAI10067). The present sequence is a peptide encoded by one

Claim 27; SEQ ID No 10662; 322pp; English.

Novel single exon nucleic acid probe used to measuring gene expression

(MOLE-) MOLECULAR DYNAMICS INC.

04-FEB-2000; 2000US-0180312. 26-MAY-2000; 2000US-0207456. 30-JUN-2000; 2000US-0608408. 30-AUG-2000; 2000US-0632366. 03-AUG-2000; 2000US-0234687. 21-SEP-2000; 2000US-0236359. 27-SEP-2000; 2000US-0236359. 04-OCT-2000; 2000GB-0024263.

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Query Match Best Local S

Similarity

40.1%; Score 686; DE 100.0%; Pred. No. 6:3 tive 0; Mismatches

6.3e-62;

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DB 22; Length 129; Indels

Conservative

16 DDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESWTEVSWPCR 75

76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135 Sequence

129 AA;

g S

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cc and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags (II). (II) is useful activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as conditional control of sites expressing (II). (I) and (II) are useful in medical cc disorders involving aberrant protein expression or biological activity. Cc diagnostics, forensics, gene mapping, identification of mutations cc anino acid sequences. Abgonolo-Aka33377 represent novel human cc assessing cc specification, but was obtained in electronic format directly from WIPO Sequence 178 AA;
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OM protein - protein search, using sw model
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Copyright (c) 1993 - 2000 Compugen Ltd
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	Drosophila me	e actual	20.0	PTP04		protein	_	Human protein sequ	Human protein SEU	Human ORFX ORF2/21	Human AC15 protein		Human polypeptide	Human polypeptide	Breast and ovarian	Novel human diagno		Human polypeptite	70	Human porypeperace		Secreted	nullan ure		Nope		Human polypeptide	Human DL162_2 Pro	secrete		acid se	cl-G p	Pentide #604 encod	=

#### ALIGNMENTS

AAE07041 ID AAE0 RESULT AAE07041 standard; Protein; 252 AA AAE07041; Human; BCL-x-like protein; therapy; physiological disorder. Human BCL-X-like protein #2. 23-OCT-2001 (first entry) Homo sapiens. 04-FEB-2000; 2000US-0180412. 31-JAN-2001; 2001WO-US03446. 09-AUG-2001. WO200157213-A2. Novel isolated human BCL-x-like polynucleotide, useful in therapeutic, diagnostic and pharmacogenic applications  $\dot{\phantom{a}}$ Donoho G, Sands AT; (LEXI-) LEXICON GENETICS INC. Claim 5; Page 32; 33pp; English. WPI; 2001-488882/53. N-PSDB; AAD13236. \_ Hilbun E, Turner CA, Friedrich G, Abuin A, Zambrowicz B;

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Novel polynucleotide encoding Bcl-G polypeptide, useful for modulating apoptosis, and for diagnosing and treating cancer .
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                                                   N-PSDB; AAH22583
                                                               WPI; 2001-398125/42
                                                                                                                 (BURN-) BURNHAM INST
                                                                                                                                            14-DEC-1999;
                                                                                                                                                               13-DEC-2000; 2000WO-US33793.
                                                                                                                                                                                                                        WO200144282-A2
                                                                                                                                                                                                                                                                                                         Human Bcl-Gs polypeptide.
                                                                                                                                                                                                                                                                        antiapoptotic;
                                                                                                                                                                                                                                                                                    Bcl-G; cancer;
                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                   AAB85167 standard; Protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human BCL-X-like protein.

The BCL-X-like polynucleotides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of protein in the body and also for treating physiological disorders and diseases. The BCL-X-like polynucleotides are useful in conjunction with polymerase chain reaction to screen libraries, isolate clones, to prepare cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 qgfpqdglmaci 252
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                                                                                        Godzik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 AA;
                                                                                                                                        99US-0461641.
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                        cancer therapy; oncogene; apoptosis; Bcl-Gs; cytostatic;
chromosome 12p12.3; human.
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Pred. No. 9.7e-131;
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         N-PSDB; AAD13235
                    WPI; 2001-488882/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                sands AT;
                                                                                                        04-FEB-2000; 2000US-0180412.
                                                                                                                                 31-JAN-2001; 2001WO-US03446.
                                                          Donoho G,
                                                                                (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                         WO200157213-A2.
                                                                                                                                                                                                                          Human; BCL-X-like protein; therapy; physiological disorder.
                                                                                                                                                                                                                                                                                                                                     AAE07040 standard; Protein; 327 AA.
                                                                                                                                                                                                                                                             Human BCL-x-like protein #1.
                                                                                                                                                                                                                                                                                           23-OCT-2001
                                                                                                                                                                                                                                                                                                                     AAE07040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methodology. Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-G specific antibodies are useful for diagnosing cancer, monitoring cancer therapy or assessing prognosis of patients with cancer. The Bcl-G polypeptides are useful for modulating the activity of an oncogenic alevel of apoptosis mediated by the Bcl-G polypeptide. They are useful for identifying modulators, for modulating composition comprising the Bcl-G polypeptide. A therapeutic is useful for treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                        241 qgfpqdglmaci 252
                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QGFPQDGLMACI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to Bcl-G polypeptides and nucleic acids encoding them. The Bcl-G polypeptides can be expressed by standard recombinant methodology. Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Fig 4; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 csaneswtevswpcrnsqssekainlgkkksswkaffgvvekedsqstpakvsaqgqrtl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 mcstsgcdleeiplddddlntiefkilayytrhhvfkstpalfspkilrtrslsgrglgn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLKTRSLSQRGLGN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt eyqdshsqqwsrclsnveqcleheavdpkvisianrvaeivyswpppqatqaggfkskei}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                         Hilbun E,
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                      Turner CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1316; DB 22; Length 252; 100.0%; Pred. No. 9.7e-131;
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                                                   Friedrich G,
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                                               Abuin A,
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                                            Zambrowicz B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 30-31; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of protein in the body and also for treating physiological disorders and diseases. The BCL-X-like polynucleotides are useful in conjunction with polymerase chain polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reaction to screen libraries, isolate clones, to prepare cloning and sequencing templates and as hybridisation probes for assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression patterns.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB85166;
                                                                                                                                                                                                                                                                07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   antiapoptotic;
                                                                                                                                                                                                                  Bcl-G; cancer;
                                                                                                                                                                                                                                        Human Bcl-Gl polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                               241 QGFPQDGL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is human BCL-X-like protein. BCL-X-like polynucleotides are useful in therapeutic, diagnostic pharmacogenic applications. They are useful for screening drugs
                                                                                                                                                       WO200144282-A2
                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGN 60
                                                                                  14-DEC-1999;
                                                                                                                                 21-JUN-2001.
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  N-PSDB; AAH22582
                                    Reed JC,
                                                           (BURN-) BURNHAM INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKDTAFIPIPLVDTSI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
            2001-398125/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                        Godzik A;
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                      cancer therapy; oncogene; apoptosis; Bcl-Gl; cytostatic; chromosome 12p12.3; human.
                                                                                      99US-0461641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 327;
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31-JAN-2000; 2000US-0179065. 04-FEB-2000; 2000US-0180628. 24-FEB-2000; 2000US-0184664. 02-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0189874.

17-JAN-2001; 2001WO-US01339.

02-AUG-2001

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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotide encoding Bcl-G polypeptide, useful for modulating apoptosis, and for diagnosing and treating cancer \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Fig 2; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis, and for diagnosing
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                                                                                                                                                                                                                                                                                                                                                                                   AAM95378 standard; Protein; 151 AA
                                                                                                                                                                                                                                                 Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                               Human reproductive system related antigen SEQ ID NO: 4036.
                                                                                                                                                                                                                                                                                                                     21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                        AAM95378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 EYQDSHSQOWSRCLSNVEQCLEHEAVDPKVISIANRVABIVYSWPPPQATQAGGFKSKEI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTL 120
                                                                                                                                                                                                                                  cancer; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 mghfqdgl 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 QGFPQDGL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 csaneswtevswpcrnsqssekainlgkkksswkaffgvvekedsqstpakvsaqgqrtl 120
                                                                                                                                                                   WO200155320-A2
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKDTAFIPIPLVDTSI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 AA;
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2000US-0215447 2000US-0218290 2000US-0220963 2000US-0224518 2000US-0224518 2000US-0225213 2000US-0225214 2000US-0225214 2000US-0225266 2000US-0225266 2000US-0225267 2000US-0225267 2000US-0225278 2000US-0225279 2000US-0225447 2000US-0225757 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0226868 2000US-0226868 2000US-0227182 30-JUN-2000; 07-JUL-2000; 07-JUL-2000;

2000US-0190076. 2000US-0198123. 2000US-0205515. 2000US-0209467. 2000US-0214886. 2000US-0215135. 2000US-021647. 2000US-021680. 2000US-0216880.

11-JUL-2000;

17-MAR-2000; 18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000;

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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used
                                                                                                                                                                                                                                                    05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                              Claim 11; SEQ ID NO 4036; 1297pp + Sequence Listing; English.
                                                                     Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                   WPI; 2001-465570/50.
N-PSDB; AAL01348.
                                                                                                                                                                                Rosen
                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 - OCT - 2000

20 - OCT - 2000

20 - OCT - 2000

01 - NOV - 2000

08 - NOV - 2000

09 - NOV - 2000

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17-NOV-2000;
17-NOV-2000;
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01-DEC-2000;
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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2000US-0256719
2000US-0251856
2000US-0251856
2000US-0251868
2000US-0251869
2000US-0251999
2000US-0251999
2000US-0254097
2000US-0254097
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2000US-0241809
2000US-0241817
2000US-0246477
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2000US-0251030.
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2000US-0240960
2000US-0241721
2000US-0241785
2000US-0241787
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2000US-0228924 2000US-0229287 2000US-0229343 2000US-0229344 2000US-0229344

14 - AUG - 2000 18 - AUG - 2000 22 - AUG - 2000 22 - AUG - 2000 23 - AUG - 2000 23 - AUG - 2000 30 - AUG - 2000 30 - AUG - 2000 30 - AUG - 2000 31 - A

2000US-023363 2000US-0233064 2000US-0233064 2000US-0234274 2000US-023499 2000US-023499 2000US-0235484 2000US-0235836 2000US-0235836 2000US-0236367 2000US-0236369 2000US-0236369 2000US-0236369 2000US-0236370 2000US-0236370 2000US-0236370 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039

08 - SEP - 2000; 14 - SEP - 2000; 15 - SEP - 2000; 16 - SEP - 2000; 17 - SEP - 2000; 21 - SEP - 2000; 21 - SEP - 2000; 22 - SEP - 2000; 23 - SEP - 2000; 26 - SEP - 2000; 27 - SEP - 2000; 27 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000;

2000US-0232400. 2000US-0232401.

2000US-0231414 2000US-0232080 2000US-0232081 2000US-0231968 2000US-0232397 2000US-0232398 2000US-0232398

2000US-0229509 2000US-0229513 2000US-0230437 2000US-0230438 2000US-0231242 2000US-0231243

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   in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB27961 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB27961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide #612 encoded by breast cell single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGN 60
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids the probes with a collection extract, and then measuring the label derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to verifying the expression of regions of gene discovery, and for encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene
                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                             New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                  Claim 27; SEQ ID NO 10929; 327pp + sequence listing; English.
                                                                                                                                                                                                                                         WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eyqdshsss-gqvlsnveqvl 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                csaneswtevswpcrnsqssekainigkkksswkaffgvvekedsqstpakvsaqgqrt1 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                            ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0633366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                  2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.5%;
95.0%;
                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 691.5; DB 2
pred. No. 5.6e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
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                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
  expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater agents of probes for measuring gene expression, with far less bias diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #639 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB33133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB33133 standard; Peptide;
                                                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 nvegclehe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 NVEQCLEHE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 DDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSORGLGNCSANESWTEVSWPCR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                   09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                           WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 25768; 639pp + sequence listing; English
                                                                                        Human genome-derived single exon nucleic acid probes useful for
                                                                                                                      WPI; 2001-483447/52.
                                                                                                                                              Penn SG,
                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nsqssekainlgkkksswkaffgvvekedsqstpakvsaqgqrtleyqdshsqqwsrcls 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                 Hanzel DK,
                                                                                gene expression in human fetal liver
                                                                                                                                                                                                   2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                        ; 2000US-0207456;
; 2000US-0608408;
; 2000US-0632366;
                                                                                                                                                                                                                                                                                 2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.1%; Score 686; DB 22;
100.0%; Pred. No. 1.7e-64;
tive 0; Mismatches 0;
                                                                                                                                                    Chen W,
                                                                                                                                                        Rank DR;
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ABB18598
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
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                                                                                      Claim 15; SEQ ID No 20368; 530pp; English.
                                                                                                                                                                                                                                                                                   26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                               WPI; 2001-488899/53.
                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00666.
                                                                                                                                                                                                                                                                        21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                     WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein #597 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB18598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB18598 standard; Protein; 129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 nsqssekainigkkksswkaffgvvekedsqstpakvsaqgqrtleyqdshsqqwsrcls 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEVQDSHSQQWSRCLS 135
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                                                                                                                                                                                        Hanzel DK,
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                                                                                                                                                                                                                                                                  2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                        2000GB-0024263
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2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 AA;
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                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.1%; Score 686; DB 22;
100.0%; Pred. No. 1.7e-64;
tive 0; Mismatches 0;
                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 129;
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AAM53929
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                                    Example 4; SEQ ID NO: 26034; 650pp + Sequence Listing; English.
                                                                                                          WPI; 2001-483446/52
                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                 03-AUG-2000;
                                                                                                                                                                                                                              30-JUN-2000;
                                                                                                                                                                                                                                                   04-FEB-2000;
                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                      WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 microarray; Alzheimer's disease; multiple sclerosis; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                            Human brain expressed single exon probe encoded protein SEQ ID NO: 26034.
                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM53929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM53929 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the hypertension, cardiac arrhythmias and congenital rearr disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 nveqclehe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 NVEQCLEHE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 nsqssekainlgkkksswkaffgvvekedsqstpakvsaqgqrtleyqdshsqqwsrcls 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 DDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESWTEVSWPCR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt 1} \ {\tt dddintiefkilayytrhhvfkstpalfspkllrtrslsqrglgncsaneswtevswpcr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                   exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                       2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                       ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.1%; Score 686; DB 22; 100.0%; Pred. No. 1.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                               schizophrenia;
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system

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                                                                                                                                                                                                                                                                                                                                                                                       PRX PF XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the probes of the invention.
                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM66317 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed probe encoded protein SEQ ID NO: 26623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM66317
                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                     WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bone marrow expressed exon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 nveqclehe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 NVEQCLEHE 144
                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 DDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESWTEVSWPCR 75
                     probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                    analyzing gene expression in human bone marrow
                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
                                                                                    The present invention provides a number of single exon nucleic acid
                                                                                                             Example 4; SEQ ID NO: 26623; 658pp + Sequence Listing; English
                                                                                                                                                                           WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                 genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                              2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                      2000GB-0024263.
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                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM14186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM14186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM14186 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #620 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 nveqclehe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 NVEQCLEHE 144
                                                            The present invention relates to human single exon nucleic acid probes (SEMP: see AAI(1068-AAI(28459). The present sequence is a peptide encoded (SEMP: see that 10068-AAI(28459). The present sequence is a peptide encoded by one such probe. The SEMPs are derived from human HeLa cells. The SEMPs by one sused to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical measuring human gene expression in a sample derived from human cervical cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 DDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESWTEVSWPCR 75
                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                         Claim 27; SEQ ID No 19012; 487pp; English.
                                                                                                                                                                                                                                                            WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt 1} \verb| dddintiefkilayytrhhvfkstpalfspkllrtrslsqrglgncsaneswtevswpcr|\\
                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.
29; Conservative
                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312.

2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-06324687.
                                                                                                                                                                                                                                                                                                                                             2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.1%; Score 686; DB 22; 100.0%; Pred. No. 1.7e-64;
                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sequence

129 AA;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Дb
                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                      Claim 27; SEQ ID No 26865; 654pp; English.
                                                                                                                                                                                                                            analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                     WPI; 2001-488897/53.
                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
            16 DDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESWTEVSWPCR 75
                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM26596 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                       27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #633 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM26596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 NVEQCLEHE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 nsqssekainigkkksswkaffgvvekedsqstpakvsaqgqrtleyqdshsqqwsrcls 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                         129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                  2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                       2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                    52.1%; Score 686; DB 22; Length 129; 100.0%; Pred. No. 1.7e-64; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.1%; Score 686; DB 22; Length 129; 100.0%; Pred. No. 1.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                   0;
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16 DDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESWTEVSWPCR 75

52.1%; Score 686; DB 22; Length 129; 10arity 100.0%; Pred. No. 1.7e-64; Conservative 0; Mismatches 0; Indels

0;

Gaps

Query Match Matches

Local

Similarity

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B
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234587.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000CB-0024263.
                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                        The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for nucleic acid expressed in the human breast. The probes are useful for
     Sequence
                                                                       predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                               Claim 27; SEQ ID No 10662; 322pp; English.
                                                                                                                                                                                                                                                                                                                         Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2001; 2001WO-US00661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #604 encoded by probe for measuring human breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM01922 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM01922;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 NVEQCLEHE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 nsqssekainlgkkksswkaffgvvekedsqstpakvsaqgqrtleyqdshsqqwsrcls 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt 1} \ {\tt dddIntiefkilayytrhhvfkstpalfspkilrtrslsqrglgncsaneswtevswpcr}
                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK, Chen W, Rank DR;
129 AA;
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RESULT
AAB85188
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                                                                                                                                                                                                                                                                                           AAB85188 standard; Protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-G; cancer; cancer therapy; oncogene; apoptosis; cytostatic;
antiapoptotic; chromosome 12p12.3; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB85188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse Bcl-G polypeptide.
                                      The invention relates to Bcl-G polypeptides and nucleic acids encoding them. The Bcl-G polypeptides can be expressed by standard recombinant methodology. Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-G specific antibodies are useful for diagnosing cancer, monitoring cancer therapy or assessing prognosis of patients with cancer. The Bcl-G polypeptides are useful for modulating the activity of an oncogenic polypeptide. They are useful for identifying modulators, for modulating polypeptide. They are useful for identifying modulators, for modulating a level of apoptosis mediated by the Bcl-G polypeptide. A therapeutic composition comprising the Bcl-G polypeptide, polynucleotide or antibody is useful for treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-1999; 99US-0461641.
                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2000; 2000WO-US33793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 NVEQCLEHE 144
                                                                                                                                                                                                                                                                                                   N-PSDB; AAH22670
                                                                                                                                                                                                                                                      Novel polynucleotide encoding Bcl-G polypeptide, useful for modulating apoptosis, and for diagnosing and treating cancer \dot{}
                                                                                                                                                                                                                                                                                                                                                                              (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                            Claim 14; Page 114-115; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
 Sequence
                            mouse Bcl-G polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                      2001-398125/42.
                                                                                                                                                                                                                                                                                                                                                    Godzik A;
    328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "encoded by NGC"
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QΥ
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      QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG65914 standard; protein; 1250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of GSK gene Id 27142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; cerebroprotective; vasotropic; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide hormone; antidiabetic; anorectic; antianorectic; antiasthmatic; antidepressant; nootropic; neuroprotectant; hypotensive; hypertensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 --TLEYQDS-HSQOWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGF 175
The invention provides polypeptides (AAG65886-65918) which may be peptide hormones (including insulin, growth hormones, chemokines, cytokines, hormones (including insulin, growth hormones, chemokines, cytokines, neuropeptides, integrins, kallikreins, lamins, melanins, notatuiretic neuropeptides, pituitary hormones, pleiotrophins, prostaglandins, secretogranins, selectins, thromboglobulins, thymosins) identified by secretogranins, selectins, thromboglobulins, thymosins) identified by high throughput genome-based biology and polynucleotides (AAI67176-67208) high throughput genome-based biology and polynucleotides (AAI67176-67208) high throughput genome-based biology and polynucleotides (AAI67176-67208) high throughput genome-based by standard recombinant encoding them. The polypeptides can be expressed by standard recombinant methodology. The polypeptides can be expressed by standard recombinant section as diabetes, breast-, prostate-, colon cancer and other malignant tumors, as diabetes, breast-, prostate-, colon cancer and other malignant tumors, hyper- and hypotension, obesity, bulinia, anorexia, growth abnormalities, hyper- and hypotension, obesity, bulinia, mental retardation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2000; 2000US-192158P.
28-MAR-2000; 2000US-192668P.
27-APR-2000; 2000US-200166P.
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                                                                                                                                                                                                                                                                                            Isolated polypeptides, which may be peptide hormones, which are identified by high throughput genome-based biology which identifies genes and gene products as therapeutic targets for treatment of diseases such as diabetes and cancer
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                                                                                                                                                                                                                                                     Claim 1; Page 91-94; 99pp; English.
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Matches 122; Query Match

Local Similarity

Conservative

33;

38.1%;

Score 501; DB 22; Pred. No. 2.5e-44; Mismatches

Length 328; Indels

24;

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Search completed: June 19, 2002, 16:34:40 Job time: 133 sec
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KEYWORDS
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1179)
Reed, J.C. and Godzik, A.
Bcl-g polypeptides, encoding nucleic
patent: WO 0144282-A 1 21-JUN-2001;
The Burnham Institute (US)
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Patent W00144282.
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Primates;
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Pred. No. 1.7e-270;
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Homo sapiens apoptosis regulator BCL-G
complete cds.
AF281254
AF281254.1 GI:125840R4
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Pines Road
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Bcl-g, a novel
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a novel pro-apoptotic member of the bcl-2
Chem. 276 (4), 2780-2785 (2001)
/note="member of Bcl-2 family"
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/product="apoptosis regulator
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196. .1179
                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                            Location/Qualifiers
                                                                  /gene="BCLG"
                                                                                                                      chromosome="12"
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/translation="MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFS
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VYSWPPPQATQAGGFKSKELFVTEGLSFQLQGHVPVASSSKKDEEEQILAKTVELLKY
SGDQLERKLKKDKALMGHFQDGLSYSVFKTITDQVLMGVDPRGESEVKAQGFKAALVI
DVTAKLTALDNHPNNRVLGFGTKYLKENFSPWIQQHGGWEKILGISHBEVD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2132)
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/db_xref="taxon:9606"
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Guo,B., Godzik,A. and Reed,J.C.
Direct Submission
                                                                                                                                                                                                   1 (bases 1 to 2039)
Guo, B., Godzík, A. and Reed, J.C.
Bcl-g, a novel pro-apoptotic member of
J. Biol. Chem. 276 (4), 2780-2785 (2001
                                                                                                                                                                                                                                                                                                                                  Homo sapiens apoptosis
complete cds.
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AF281255.1 GI:12584086
                                                                                                                Submitted (22-JUN-2000) The Burnham Pines Road, La Jolla, CA 92037, USA
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Mammalia; Eutheria; Primates;
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Donoho,G., Hilbun,E., Turner,C.A., Friedrich,G.B., Abuin,A.,
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Montpetit, A., Boily, G. and
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                                Eukaryota; Metazoa; Chordata; Craniat Mammalia; Eutheria; Primates; Catarrh (bases 1 to 954)
Reed, J.C. and Godzik, A.
Bcl-g polypeptides, encoding nucleic Patent: WO 0144282-A 3 21-JUN-2001;
The Burnham Institute (US)
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/db_xref="G1:14598302"
/db_xref="G1:14598302"
/translation="McSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHYFKSTPALFS
/translation="McSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHYFKSTPALFS
PKLLRTBSLSQRGLGNCSANESWTEYSWPCRNSQSSEKAINLGKKKSSWKAPFGVVEK
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VYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHYPVASSSKKDEEEQILAKIVELLKY
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                             gagaaggccataaaccttggcaagaaaagtcttcttggaaagcattctttggagtagtg
                                                              aacgtggagcagtgcttggagcatgaagctgtgggaccccaaagtcatttccattgccaac 465
                                                                                                                                                                                                                                                                                                                  gaga---aggaagattcgcagagcacgcctgccaaggtctctgctcagggtc-----
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aagtccaaagagatttttgtaactgagggtctctcccttccagctccaaggccacgtgcct 585
                                                                                                                            AGTGTGGAGCAG - CCCTGGAGAGTGAAGTTGTGGATTCCAAAGTGGCTTGTATTGCCAAC
                                                                                                                                                                                                           CCCTTCCCGGTAGAGCGGCAGAGTGGCTTCCACAACCAGCACTGGCCCCAGGTCTCTGAGC 417
                                                                                                                                                                                                                                ----aaaggacgttggaataccaagattcgcacagccagcagtggtccaggtgtctttct
                                                                                                                                                                                                                                                                                            GAGAAGGAGGAAGGCCTGCCGNGCTCCCCAAAGGAGATCCGAGCTCAGGGTCCTCAGGGC
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                                            AGAGTGGCTGAAATTGTTTACTCCTGGCCACCACCAGATGTCATCCACAGCCAGGGAGGA 536
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Patent: WO 0144282-A 41 21-JUN-2001;
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IDAIAKLTASDNHPMNRMLGFGTKYLKEYFSPWVQQNGGWEKILGISHEEVD"
1 246 c 271 g 197 t 1 others
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EGLPXSPKEIRAQGPQGPFPVERQSGFHNQHWPRSLSSVEQPWRVKLWIPKWLVLPTE
WLKLFTPGHHQMSSTAREEASSKRGSRRFLYFRFEGPWDSKNKDGEDQIISKIVELLK
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         Submitted (28 MAY-1999) Human Genome Sec
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                     Submitted (27-MAY-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                  Direct Submission
Submitted (13-MAY 1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, US. 3 (bases 1 to 190858)
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AUTHORS TITLE JOURNAL

Worley, K.C.
Direct Submission

Submitted (09-OCT-1999) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On May 28, 1999 this sequence version replaced gi:4895156.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Department

gc-help@bcm.tmc.edu

COMMENT

sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts.
Repeats are identified using RepeatMasker (A. Res. 7:541-5 from dbSTS, 7:541-550) searches GDB, and

Smit and P. Green,

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the as Low Coverage.

quality at URL: QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT--

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 194143)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome 12 clone SEQUENCE, 26 unordered minor
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Pred. No. 1.4e
O: Mismatches
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. 1.4e-113;
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RP11-525I3, WORKING
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Hollins, B., Homaif, F., Howard, S., Huber J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mahreshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Macker, M., Miner, Z., Mitchell, T., Mehabbat, K., Morgan, M., Morris, S., Moser, M., Nickerson, E., Nwokenkwo, S., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., P., L., Quilaes, M., Ren, Y., Rives, M., Rojubokan, I., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Shorsh, S., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tangy, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tahley, R., Ward-Moore, S., Warten, R., Washington, C., Wartin, R., Washington, C., Wartin, R., Washington, C., Wartin, R., Washington, C., Wall, Lans, G., Williams, G., Williamson, A., Waleczyk, R., Wooden, S., Warten, R., Washington, C., Mu, Y., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley,K.C.
Direct Submission
Submitted (27-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 25, 2001 this sequence version replaced g1:13957543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Enster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Gazza, N., Gil, R., Gorrell, J.H., Guevara, W., Gunarthe, P., Hale, S.
                                                                                                                                                                                                                                                                                                              Center clone name: RP11-52513

Sequencing vector: Plasmid; M77789

Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 7% of reads
Chemistry: Dye-terminator Big Dye: 93% of reads
Chemistry: Dye-terminator Dye: 10,000 Dye: 10,000 Dye: 10,000 Dye: 10,000 Dye-termination
Consensus quality: 208935 bases at least Q30
Estimated insert size: 199196; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
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Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.
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Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
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  21476: contig of 21476 bp in length 21576: gap of unknown length
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Best Local Similarity
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121 gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaat 180
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                                                                                                                                                                                  1 atgtgtagcaccagtgggtgtgacctggaagaaatccccctagatgatgatgacctaaac 60
                                                                                            accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct 120
                                                                                                                                                           ATGTGTAGCACCAGTGGGTGTGACCTGGAAGAAATCCCCCCTAGATGATGATGACCTAAAC
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/db_xref="taxon:9606"
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Pred. No. 1.4e-113;
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JOURNAL REFERENCE AUTHORS TITLE JOURNAL

TITLE

Unpublished Direct Submission

(bases 1 to 194143)

COMMENT

Center project name: HABL

Center code: BCM

Genome Center

be preserved

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RESULT 1
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CE 1 (bases 1 to 200499)

RS MUZNY, D. M., Adams, C., Adio-Oduola, B. Ali-Osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Barks, T., Barbaria, J., Benton, J., Blimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryard, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, E., Brown, M., Bryard, N.C., Chern, G., Chew, J., Charley, R., Burnell, K.L., Byrd, N.C., Carron, T.F., Chen, Z., Chowdhy, I., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, Z., Chowdhy, I., Dederich, D.A., Delaney, K.R., Delgado, O., Day, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Eggar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferragutto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Galisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Joudh, S., Kallsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Loulseged, H., Lozado, R.J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lucier, A., Wartindale, A., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mahabbat, K., Martin, C., Wetzker, M., Mapua, P., Martin, R., Martindale, A., Martindale, A., Naguyen, N., Nguyen, N., Newtson, N., Newtson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 16, 2001 this sequence version replaced gi:15042773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 20551 bases at least Q40

Consensus quality: 207841 bases at least Q30

Consensus quality: 208973 bases at least Q30

Estimated insert size: 203052; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; sum-of-contigs estimation Quality coverage: 12.7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                             /clone="RP11-525I3"
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/chromosome="12P"
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97.4%;
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Score 435.8; DB 2;
Pred. No. 1.4e-113;
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                             agaaagctgaagaaagataaggctttgatgggccacttccaggatgggctgtcctactct 732
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                  ACACAGCTGAAGAAAGATAAGGCTTTGATGGGCCACTTCCAGGATGGGCTGTCCTACTCT 357
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Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                  NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens cDNA FLJ20120 fis, AK000127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-FEB-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
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                                                                                                                                         /tissue_type="colon"
/note="cloning vector
404 c 342 g
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="COL05912"
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                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                      21.9%;
98.2%;
                      Score 215.6; DB 9
Pred. No. 1.3e-50;
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Direct Submission
Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064657.
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findPhrapList
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NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 114307 bases at least Q40 Consensus quality: 121845 bases at least Q30 Consensus quality: 128763 bases at least Q20 Estimated insert size: 114370; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-177C11
------Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
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96126	AGATCCATGCTCAGGGCCCCTTCCCGGTAGAGCGGCAGGGTAGGAACCAGCACTGGT	96182	Db	
391	aggtctctgctcagggtcaaaggacgttggaataccaagattcgcacagccagc	332	Qy	
96183	2 CTTGGAGAACACTCTTCAGAGTAACAGAGAAGGAAGGAGCCGCCGAGCTCCCCAAAGG	9624	Дb	
331	275 cttggaaagcattctttggagtagtggagaaggaagattcgcagagcacgcctgcca 331	279	Qy	
962	96302 TGCCCTGTAGAGATTCCCTCTCCAGTGAAAAGCACATAAGCTTGGGCAAGAAGAAGTCTT 96243	96302	Db	
274	5 ggccttgcagaaattcccaatccagtgagaaggccataaaccttggcaagaaaaagtctt	215	Qy	
96303	GTTTGTCCCAGAAAGCACTGGGGACTTGGTCAACTGACTCCTGGACACAGATATCGT	96359	DЪ	
214	gtttgtcccagaggggcctggggaattgttcagcaaatgagtcatggacagaggtgtcat	155	Qy	
96360	GACACCATGTCTTCAAGAGCCCCCCGGCTGTCTTCTCCCCCCAAGCTCTCCAGGACCAGAA	96419	Db	
154	5 gacatcatgtcttcaagagcacccctgctcttcttctcaccaaagctgctgagaacaagaa	95	Qy	
96	96479 CCCCCTGGAGGGCGATGATCGGACCAGCATAGAGTTCAAAAATCCTGCCGTTTTATGCCA 96420	96479	Db	

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Human BCL-X-like p
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Human Bcl-X-like p
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Human BCL-X-like p
Human Bcl-Gs polype
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ABA04982 ABA32090 AAK13408 AAK13408 AAK13408 AAK13954 AAI1954 AAI19566 AAA1552 AAI107666 AAA22153 AAK00629 AAI10708 AAK131966 AAA3110708 AAI10708 AAI10709
Human roctal liver probe #10556 for get human brain expres Human brain expres Human brain expres #9887 for get probe #13838 used probe #13838 used probe #657 used to human foetal liver probe #619 for gen human brain expres Human Bcl-Gs mutagenic p sequence of phage sequence of phage sequence of phage porcine reproducti Human Bcl-X-like p Human bcl-Gl polyp Human bcl-Gl polyp Human bcl-Gl polyp Human brain expres probe #7360 for get Human brain expres Human brain express Human Brai

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		Donoho G, Hilbun E, Turner CA, Friedrich G, Abuin A, Zambrowicz B;		(LEXI-) LEXICON GENETICS INC.		04-FEB-2000; 2000US-0180412.		31-JAN-2001; 2001WO-US03446.		09-AUG-2001.		WO200157213-A2.		<pre>/product= "Human BCL-X-like protein #1"</pre>	/*tag= a	1984	Key Location/Qualifiers 人		Homo sapiens.		Human; BCL-X-like protein; therapy; physiological disorder; ss.		Human BCL-X-like protein encoding cDNA #1.		23-OCT-2001 (first entry)		AAD13235;		AAD13235 standard; cDNA; 984 BP.	3235

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The invention relates to Bcl-G polypeptides and nucleic acids encoding them. The Bcl-G polypeptides can be expressed by standard recombinant methodology. Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-specific antibodies are useful for diagnosing cancer, monitoring cancer therapy or assessing prognosis of patients with cancer. The Bcl-G polypeptides are useful for modulating the activity of an oncogenic polypeptide. They are useful for identifying modulators, for modulating a level of apoptosis mediated by the Bcl-G polypeptide. A therapeutic composition comprising the Bcl-G polypeptide, polynucleotide or antibod is useful for treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a CDNP
                                                                                                                                                                                                                                                                                                                                                            Claim 3;
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           ctgaaagagaacttctcgccatggatccagcagcacggtggatgggaaaaaatacttggg
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a cDNA encoding human BCL-X-like protein. The BCL-X-like polynucleotides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of protein in the body and also for treating physiological disorders and diseases. The BCL-X-like polynucleotides are useful in conjunction with polymerase chain reaction to screen libraries, isolate clones, to prepare cloning and sequencing templates and as hybridisation probes for assessing gene expression patterns.
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Sands AT;
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       food supplement;
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      medical imaging;
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23-AUG-2000;
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerased are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful in treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed confidence of the companion of the printed confidence of the companion of the confidence of the companion of the confidence of the companion of the confidence of t
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                                   BCL-X-like
                                                                                   (first entry)
                                 protein;
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                                 therapy; physiological
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                                 disorder;
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Sands AT;
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                  The invention relates to Bcl-G polypeptides and nucleic acids encoding them. The Bcl-G polypeptides can be expressed by standard recombinant methodology. Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-G specific antibodies are useful for diagnosing cancer, monitoring cancer therapy or assessing prognosis of patients with cancer. The Bcl-G polypeptides are useful for modulating the activity of an oncogenic polypeptide. They are useful for identifying modulators, for modulating a level of apoptosis mediated by the Bcl-G polypeptide. A therapeutic composition comprising the Bcl-G polypeptide, polypeptide or antibody is useful for treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a cDNA
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antiapoptotic;
          encoding
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          a Bcl-Gs
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chromosome 12p12.3; human; ss.
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          polypeptide
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Best Local Similarity
Matches 677; Conserv
                                                                                                                      Bcl-G; cancer;
antiapoptotic;
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                                                                                                                      cancer therapy; oncogene; apoptosis;
chromosome 12p12.3; mouse; ss.
  Location/Qualifiers 1..987
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Pred. No. 3.9e
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific antibodies are useful for diagnosing cancer, monitoring cancer therapy or assessing prognosis of patients with cancer. The Bcl-G polypeptides are useful for modulating the activity of an oncogenic polypeptide. They are useful for identifying modulators, for modulating a level of apoptosis mediated by the Bcl-G polypeptide. A therapeutic composition comprising the Bcl-G polypeptide, Polypucleotide or antibody is useful for treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to Bcl-G polypeptides and nucleic acids encoding them. The Bcl-G polypeptides can be expressed by standard recombinant methodology. Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 987 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 114-115; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis, and
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aacgtggagcagtgcttggagcatgaagctgtggaccccaaagtcatttccattgccaac
                                  cccttcccggtagagcggcagagtggcttccacaaccagcactggcccaggtctctgagc
                                                    ----aaaggacgttggaataccaagattcgcacagccagcagtggtccaggtgtctttct
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
 28-JUN-2000;
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07-JUL-2000;
                                                                                                                                31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL01348 standard;
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0204867.
2000US-0214886.
2000US-0215135.
2000US-0215135.
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2000US-0184664.
2000US-0186350.
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2000US-0225266
2000US-0225447
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11-JUL-2000; 11-JUL-2000; 11-JUL-2000; 14-JUL-2000; 26-JUL-2000; 26-JUL-2000; 14-AUG-2000; 14-AUG-2000;

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20-CCT-2000

01-NOV-2000

08-NOV-2000

017-NOV-2000

117-NOV-2000

117-NOV
                                               The present invention provides the protein and coding sequences of number of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the invention.
  Sequence
                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                 Isolated nucleic is used in preven
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-465570/50.
P-PSDB; AAM95378.
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  632 BP;
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2000US-0246475

2000US-0246477

2000US-0246477

2000US-0246673

2000US-0246528

2000US-0246528

2000US-0246528

2000US-0246610

2000US-0246611

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2000US-0249211

2000US-0249214

2000US-0249216

2000US-0249217

2000US-0249218

2000US-024928

2000US-0251188

2000US-02511898

2000US-02511989

2000US-02511989

2000US-02511999

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2000US-0241826.
2000US-0244617.
                                                                                                                                                                                                          ID NO 1349; 1297pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENOME
  190
  Α.
                                                                                                                                                                                                                                                           molecule encoding a reproductive system antigen , treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben
  143
C;
                                                                                                                                                                                                                                                                                                                                                                                                                               , MS
  166
                                                                                                                                                                                                            Sequence Listing; English.
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  128
  Η.
5 other;
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22-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

114-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-CCT-2000 29-CCT-2000

2000US-0233065
2000US-0234223
2000US-0234297
2000US-0235834
2000US-0235836
2000US-0235836
2000US-0236327
2000US-0236368
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Best Local
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 04-FEB-2000;
26-MAY-2000;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                      Homo
                                                                                                                                                                                             disease; cancer;
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                                                                                                                                                                                                                                                                               ABA47100;
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                                                                                                30-JAN-2001;
                                                                                                                                             WO200157271-A2
                                                                                                                                                                                                         Human;
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                                                                                                                                                                                                       microarray; single
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-06323687.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                               2001WO-US00662
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Pred. No. 2.1e-124;
D; Mismatches 54;
                                                                                                                                                                                                       probe;
                                                                                                                                                                                                       gene
                                                                                                                                                                                                       expression; breast;
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Matches Query Match Best Local

Similarity

39.4%; 100.0%;

Score 388; Pred. No.

Mismatches

1.3e-111;

DB 22;

Length 388;

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The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC bound to each probe of the microarray. The probes are useful for CC verifying the expression of regions of genomic DNA predicted to CC determining predisposition and/or prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical CC agents on cells. The microarray of this invention presents a far greater CC diversity of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for CC rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. CC Note: The sequence data for this pattent did not form part of the CC printed specification, but was obtained in electronic format directly cxx
Sequence 388 BP; 113 A; 91 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 5795; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New spatially-addressable set of single exon nucleic acid probes,
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                 aacgtggagcagtgcttggagcatgaag 433
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aacgtggagcagtgcttggagcatgaag
                                                               ttctttggagtagtggagaaggaaggattcgcagagcacgcctgccaaggtctctgctcag
                                                                                                                                                                                                                 aattcccaatccagtgagaaggccataaaccttggcaagaaaaagtcttcttggaaagca
                                                                                                                                                                                                                                                                   aggggcctggggaattgttcagcaaatgagtcatggacagaggtgtcatggccttgcaga
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                                                                                                                                                                                                                                                                                                                                                                                                                  gatgatgacctaaacaccatagaattcaaaatcctcgcctactacaccagacatcatgtc 105
                                                                                                                                 ttctttggagtagtggagaaggaagattcgcagagcacgcctgccaaggtctctgctcag
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 388
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                   ches
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 13287; 639pp + sequence listing; English.
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                                                 ttctttggagtagtggagaaggaaggattcgcagagcacgcctgccaaggtctctgctcag
                                                                                    aattcccaatccagtgagaaggccataaaccttggcaagaaaaagtcttcttggaaagca
                                                                                                                                     aggggcctggggaattgttcagcaaatgagtcatggacagaggtgtcatggccttgcaga
                                   ttctttggagtagtggagaaggaattcgcagagcacgcctgccaaggtctctgctcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                 Similarity
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2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                    Conservative
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2000US-0207456.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid probes useful
liver -
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                                                                                                                                                                                                                                                                                   Gaps
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Query Match
Best Local Similarity
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
27 - SEP - 2000;
                                                                                                                                         Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                       probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                        measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single
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26-MAY-2000;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure genomic set pression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                 The
                                                                                                                                                                                                                                                                                                                                   WPI;
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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brain expressed single exon
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                                                                                                                                                                                                                Example 4;
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                                                                                                                                                               present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                     microarray;
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mes 388; Conser
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                                        sg,
                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                    aggggcctggggaattgttcagcaaatgagtcatggacagaggtgtcatggccttgcaga
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                       2001-488900/53.
                                                                                                                                                                                                             bone marrow
                                                       MOLECULAR DYNAMICS
                                       Hanzel
                                                                                                                                                                                                      cancer; leukaemia;
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                                                                     2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                      2001WO-US00668
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                       DK,
                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                             expressed exon;
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                                        Chen
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                        Rank
                                                                                                                                                                                                      lymphoma; myeloma;
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                                                                                                                                                                                                                                                                                                                                     433
                                                                                                                                                                                                             gene expression analysis;
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                                        DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T; 0 other;
                                                                                                                                                                                                                             probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                             SEQ ID NO: 13702.
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                                                                                                                                                                                                             probe;
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analyzing gene expression

Human genome-derived single exon nucleic acid

in human

bone marrow

probes

useful

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AAI19954
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Best Local S
Matches 388
 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                AAI19954 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                          Probe; human; cervical canc
                                                                                                                                                                                                                                                         AAI19954;
                                                                                30-JAN-2001;
                                                                                                                               WO200157278-A2
                                                                                                                                                                                                          Probe #9887 for gene expression
                                                                                                                                                                                                                                   12-OCT-2001
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                                                                                                                                                     Homo sapiens
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                                                                                                                                                                            cancer;
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2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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llarity 100.0%;
Conservative
                                                                                2001WO-US00670
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                    microarray;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658pp + Sequence Listing;
                                                                                                                                                                                     expression;
                                                                                                                                                                                                           analysis in
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1.3e-111;
                                                                                                                                                                                     cervical
                                                                                                                                                                                                           human
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                                                                                                                                                                                                           cervical cell sample
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                                                                                                                                                                                     epithelial cell;
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ID AAI4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC
                                                                                                             AAI45152;
                                                                                                                                         AAI45152 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 388 BP; 113 A; 91 C; 99 G; 85 T; 0 other;
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les 388; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                          aacgtggagcagtgcttggagcatgaag
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zing gene expression in
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                                                                                 (first entry)
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genetic disorder; Probe; microarray; human;

S

placenta;

antenatal diagnosis

Probe

#13838

used to measure

gene

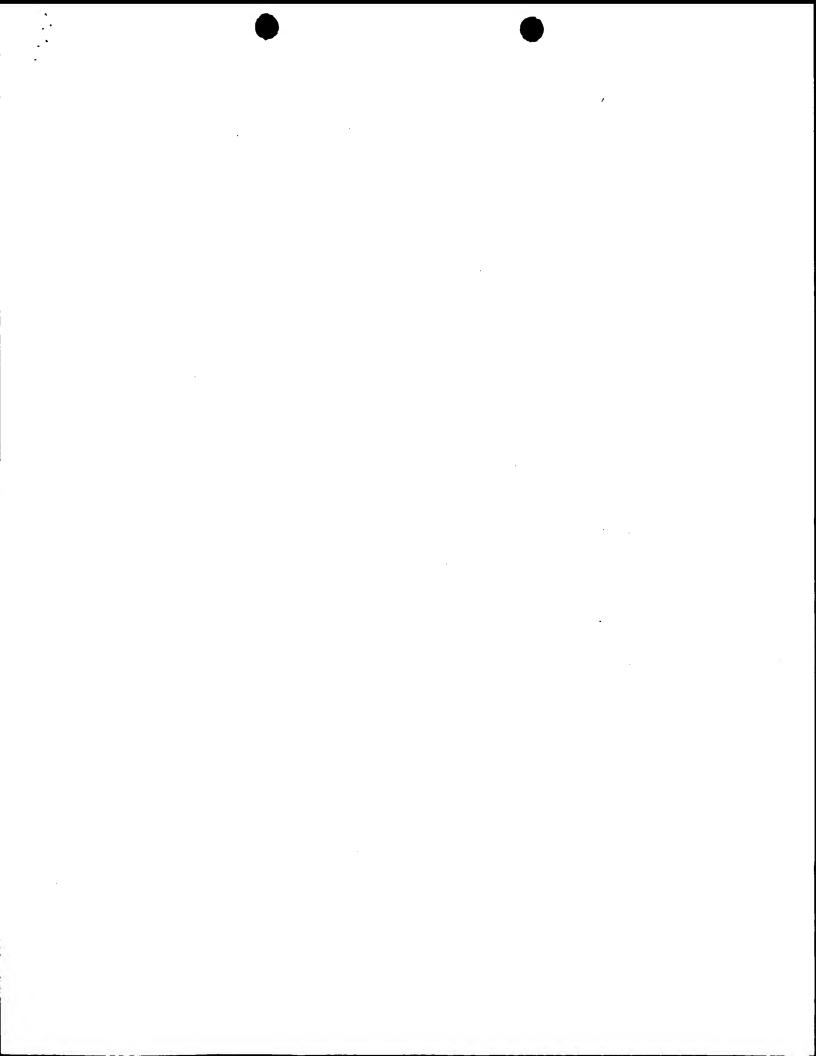
expression in human placenta sample

Homo sapiens.

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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes in the present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying goexpression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
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Search completed: June 20, Job time: 5973 sec

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## ALIGNMENTS

RESULT 1 BI833102	
LOCUS	BI833102 980 bp mRNA linear EST 04-OCT-2001
DEFINITION	603090814F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5229819 5',
ACCESSION	BIB33102
VERSION	BI833102.1 GI:15944652
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	1 (bases 1 to 980)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-r@mail.nih.gov
	CDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LLAM11578 row: k column: 04
FEATURES	Location/Qualifiers
source	1980
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:5229819"
	/clone_lib="NIH_MGC_120"
	/lab_host-"DH10B"
	<pre>/note="Organ: pooled pancreas and spleen; Vector:</pre>
	<pre>pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA</pre>
	source anonymous pool of spleen and pancreas from 28 yo
	male. Library is oligo-dT primed and direction
	(EcoRV site is destroyed upon cloning). Average insert
	size 1.5 kb, insert size range 1–2.5 kb. Library is

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                                                     BG718587
602696672F1 NIH_MGC_97
                                 mRNA sequence.
BG718587
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ttggagcatgaagctgtggaccccaaagtcatttccattgccaaccgagtagctgaaatt
                                                              gaataccaagattcgcacagccagcagtggtccaggtgtctttctaacgtggagcagtgc
                                                                                                                          gagaaggaagattcgcagagcacgcctgccaaggtctctgctcagggtcaaaggacgttg
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                                                                                                                                                                                                                                                                                                                                                                    accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct 120
                                               GAATACCAAGATTCGCACAGCCAGCAGTGGTCCAGGTGTCTTTCTAACGTGGAGCAGTGC
                                                                                                          GAGAAGGAAGATTCGCAGAGCACGCCTGCCAAGGTCTCTGCTCAGGGTCAAAGGACGTTG
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10747 row: o column: 17
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
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National Institutes of Health, Mammalian
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1 (bases 1 to 763)
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/clone_lib="NIH_MGC_97"
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/db_xref="taxon:9606"
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609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10736 row: m column: 17
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
I (bases 1 to 774)
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602692271F1 NIH_MGC_97
                                                                                                                      Similarity
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                                                                                                        Conservative
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                                                                                                                                                                                        /note="organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BanHI; Site_2: SalI-XhoI (gtcg); Oligo-dT primed using primer 5'-TTTTTTTTTTTVN-3; Size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:4824760"
/clone_lib="NIH_MGC_97"
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                                                                                                                      55.8%;
98.1%;
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Pred. No. 1.1e~143;
D; Mismatches 5;
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MEDLINE
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Shibata,K., Itoh,M., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Konno,H., Akiyama,J., Nishi,K., Ritsunai,T., Nishine,T., Harada,A., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Sumi,N., Ishii,Y., Nakamura,S., Ikazama,M., Nishine,T., Kashiwagi,K.,
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                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new captains.
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Carninci,P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Figure Visit our web site (http://genome.gsc.riken.go.jp/) for finester visit our web site (http://genome.gsc.riken.go.jp/)
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                                                                                                                                                                                                                      /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amHI. Host: DH10B.
Location/Qualifiers
                     /protein_id="BAB30545.1"
/db_xref="GI:12856034"
                                                                                                                                      /note="BCL2-like apoptosis inhibitor containing protein
data source:InterPro, source key:IPR002475, evidence:IS
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="4933430L01"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="MGD:MGI:1894677"
translation="MCSTSVYDLEDIPLEDDDPNSIEFKILAFYARHHVFKNTPAVFS"
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VAEIVYSWPPPDVIHSQGSKLKERVSEILYRFREGFCDSKNKDGEDQIISKIVELLK
FSGDQLGREIKKDKALMSSFQDGLSYSTFKTITDLFLRDVDTRGESEVKARGFKAALA
IDAIAKLTAIDNHPMNRMLGFGTKYLREYFSPWVQQNGGWEKILGISHEEVD"
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Matches

742;

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Similarity

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                                                                                           Adachi, Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Fukuno, M., Hanagaki, T., Hara, A., Hayatsu, M., Hil, D., Hiramoto, K., Hiraka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojina, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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1541 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210008009:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409, 685-690 (2001)
5 (bases 1 to 1541)
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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GAAAAGAACATCAGCTTGGGCAAGAAGAAGTCTTCTTGGAGAACACTCTTCAGGGTGGCC
                      TGGT---CAACTGATTCCTGGACACAGGTATCATTGCCTTGCAGAGGTTCCCCCCTCCAGC 410
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Please visit our web site (http://genome.gsc.riken.go.jp/)
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/dev_stage="adult"
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/db_xref="GI:12843026"
/translation="MCSTSVYDLEDIPLEDDDDPNSIEFKILAFYARHHVFKNTPAVFS
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High-efficiency full-length cDNA cloning
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  Shibata,Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.gsc.riken.go.jp/)
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/tissue_type="colon"
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/db_xref="GI:12858358"
/db_xref="GI:12858358"
/translation="MCSTSYVDLEDIPLEDDDPNSIEFKILAFYARHHVFKNTPAVFS
PKLSRTRSLSQKALGTWSTDSWTQVSLPCRGSPSSEKNISLGKKKSSWRTLFRVAEKE
EKLPSSPKEIRAGGPGGPFPVERQSGFHNQHWPRSLSSVEQRLESEVVDSKVACIANR
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Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagak
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., H
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                                                                                                                              Nature 409, 685-690 (2001) 5 (bases 1 to 2222)
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Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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                    Itoh, M., Izawa, M., Kasukawa, T.,
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VAEIVYSWPPPDVIHSQGGSKLKERVSEILYFRFEGPCDSKNKDGEDQIISKIVELLK
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/translation="MCSTSVYDLEDIPLEDDDPNSIEFKILARYARHHYFKNTPAVFS
PKLSRTRSLSQKALGTWSTDSWTQVSLPCRGSPSSEKNISLGKKKSSWRTLFFKVAEKE
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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               mRNA sequence.
BI838169
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603083677F1 NIH_MGC_120
B1838169.1
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                                                    Homo
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                                                  clone IMAGE:5222875
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FEATURES

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/sex="male"

/codon\_start=1

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TITLE JOURNAL

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/note="putative" 565 c 551

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ttggagcatgaagctgtggaccccaaagtcatttccattgccaaccgagtagctgaaatt
                                                                                                                                                                                                              GAATACCAAGATTCGCACAGCCAGCAGTGGTCCAGGTGTCTTTCTAACGTGGAGCAGTGC
                                                                gaataccaagattcgcacagccagcagtggtccaggtgtctttctaacgtggagcagtgc 420
                                                                                                                                                                                                                                                                                                   TGTTCAGCAAATGAGTCATGGACAGAGGTGTCATGGCCTTGCAGAAATTCCCAATCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11560 row: i column: 20
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Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 715)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"organ: pooled pancreas and spleen; vector:
/note-"organ: pooled pancreas and spleen; vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

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/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
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      181
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                                                                                                                       gtttattcctggccaccaccacaagcgacccag 513
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tgttcagcaaatgagtcatggacagaggtgtcatggccttgcagaaattcccaatccagt 240
                                                                  gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagagggggcctgggggaat 180
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                                            GCTCTCTTCTCACCAAAGCTGCTGAGAACAAGAAGTTTGTCCCAGAGGGGCCTGGGGAAT 338
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Tissue Procurement: Miklos Palkovits,
cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 672)
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BG717835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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Plate: LLAM10740 row: m column:
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag ); Oligo-dT primed using primer 5'-TTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 162 c 171 g 142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:4826292"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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Pred. No. 4.3e-129;
0; Mismatches 3;
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Brownstein (NHGRI),
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                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM11540 row: j column: 19
High quality sequence stop: 701.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 703)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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603066277F1 NIH_MGC_118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                          208
                                                                     /note-"Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NHH_MGC Library."
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sapiens cDNA clone IMAGE:5215218 5',
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AW000827.1
EST.
                                                                                                                                                                                             Uppublished (1997)
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW000827
426 bp mRNA linear EST 09-MAR-20 wu45dl0.xl Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522995 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Euthería;
                                                                                                                                                                      Tumor Gene Index
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                 /clone="IMAGE:2522995"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
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disease"
                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                      Location/Qualifiers
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D; Mismatches 1;
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                                                                                                                                                                                                                                                    mRNA sequential BI652080
Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cyapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Dencon Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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603298866F1 NIH_CGAP_Mam3 Mus
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 676)
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RESULT COCUS

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aagtagactga 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: this is a NCI_CGAP Library."
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/db_xref="taxon:10090"
/clone="IMAGE:5339464"
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/lab_host="DH10B"
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Pred. No. 3.9e-90;
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                                                                                                            CCATAAACCTTGGCAAGAAAAAGTCTTCTTGGAAAGCATTCTTTGGAGTAGTGGAGAAGG
             atgaagctgtggaccccaaagtcatt
                                                              aagattcgcacagccagcagtggtccaggtgtctttctaacgtggagcagtgcttggagc 427
                                                                                                                                                                                                                                            CATATGAGTCATGGACAGAGGTGTCATGGCCTTGCAGAAATTCCCAATCCAGTGAGAAGG
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                                               AAGATTCGCACAGCCAGCAGTGGTCCATGTGTCTTTCTAACGTGGAGCAGTGCTTGGAGC
                                                                                                                                                                                                                                                                                                             TCTCACCATAGCTGCTGAGAACAAGAAGTTTGTCCCACAGGGGCCCTGCGGAATTGTTCAG
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: jwallace@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC,
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Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
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/db_xref="taxon:9606"
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Pred. No. 1.3e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jappel: 81-45-503-9222
Tel: 81-45-503-9216
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RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahari,Y. and Hayashizaki,Y.
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)

On Jun 1, 2000 this sequence version replaced gi:8136849.

Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizav
                                                                                                                                                                                                                               prepare mouse tissues
                                                                                                                                                                                                                                                              Division of Experimental Animal
                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse
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                              /db_xref="taxon:10090"
/clone="4930470009"
                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
/clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:16257339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         furuno,M., Hanagaki,T., Hara,A.
to,M., Kawai,J., Konno,H., Kouda
   enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanaka, T., Matsuura
   adult male testis
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              608 atgaagaagaacaatactagccaaaattgttgagctgctgaaatattcaggagatcagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 gattcgcacagccagcagtggtccaggtgtctttctaacgtggagcagtgcttggagcat 429
                                                                                                                                                                       579
                                                                                                                                                                                                                                                                                                                                                                                  728
                                                                                                                                                                                                                                                                                                                                                            actctgttttcaagaccatcacagaccaggtcctaatgggtgtggaccccaggggagaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTACAACAACCAGCACTGCCCCAGGTCTCTGGGCAGTGTGGAGCAGCGCCTGAAGAGT 170
                                                                                                                                                                                                                                                  CAGAGGTCAAAGCTCGGGGCTTCAAGGCTGCCCTTGCAATAGACGCCCATCGCCAAGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGTTTGTAGATTCCAATGTGGCTTGTATAGCCAACAGAGTGGCTGAAATTGTTAACTCC
                                                                                                                                                                                                                                                                        cagaggtcaaagctcagggctttaaggccttgtaatagacgtcacggccaagctca
                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGAAGAGAGATAAAGAAAAGACAAGGCTTTGATGAGCAGCTTCCAGGACGGGCTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctgagggtctctccttccagctccaaggccacgtgcctgtagcttcaagttctaagaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaagctgtggaccccaaagtcatttccattgccaaccgagtagctgaaattgtttattcc 489
                      atgaagaagtagactga 984
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                                                                                                     agaacttctcgccatggatccagcagcacggtggatgggaaaaatacttgggatatcac
                                                                                                                                                                 CGGCCATCGACAACCACCCAATGAATAGAATGCTGGGCTTCGGGGACCAAGTACCTAAGAG
                                                                                                                                                                                       cagctattgacaaccacccgatgaacagggtcctgggctttggcaccaagtacctgaaag
                                                                                                                                                                                                                                                                                                                                      ACTCAACGTTCAAGACCATCACAGACCTGTTCCTGAGGGACGTGGACACCAGAGGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAGAAGACCAAATAATAAGCAAGATTGTTGAGCTGCTGAAATTCTCGGGGGATCAGT
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ATGAAGAAGTAGACTGA 715
                                                                               AGTACTTCTCCCCCTGGGTTCAGCAGAATGGCGGATGGGAAAAAATACTTGGGATCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Rike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
/note="Site_1: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="testis"
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76.8%;
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Pred. No. 1.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                       Н
                                                            ttgttcagcaaatgagtcatggacagaggtgtcatggccttgcaga-aattcccaatcca 238
                                                                                                                                                                                                                                 accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct 120
                                                                                                                                                                                                                                                                                                                 atgtgtagcaccagtgggtgtgacctggaagaaatccccctagatgatgatgacctaaac 60
gtgagaaggccataaaccttggcaagaaaagtcttcttggaaagcattctttggagtag
                                                                                                                                              gctct-cttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaa 179
                                         TTGTTCAGCAAATGAGTCATGGACAGAGGTGTCATGGCCTTGCAGANAATTCCCAATCCA
                                                                                                                                                                                                             ACCATAGAATTCAAAATCCTCGCCTACTACACCAGACATCATGTCTTCAAGAGCACCCCT 171
                                                                                                                                                                                                                                                                                             ATGTGTAGCACCAGTGGGTTGCACCTGGAAGAATCCCCCCTAGATGATGATGACCTAAAC 111
                                                                                                                           GCTCTGCTTCTCACCAAAGCTGCTGAGAACAAGAAGTTTGTCCCAGAGGGCCATGGGGAA
                                                                                                                                                                                                                                                                                                                                                                                347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA399486 406 bp mRNA linear Ezt60c07:rl Soares_testis_NHT Homo sapiens cDNA clone 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence. AA399486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and wentstructed by Bento Soares and M. Fatima Bonaldo. "95 c 101 g 82 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:726732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:5923643"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                 32.7%;
97.7%;
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                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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E IMAGE:726732
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- ДЬ 292 GTGAGAAGGCCATAAACCTTGGCAAGAAAAGTCTTCTTGGAAAGCATTCTTTGGAGTAG 351
- P Q

Search completed: June 20, 2002, 04:19:16 Job time: 6406 sec

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Run on:
                                                                                                 OM protein - protein search, using sw model
June 19, 2002, 16:33:47; Search time 15.65 Seconds (without alignments) 809.028 Million cell updates/sec
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                   Compugen Ltd.
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Title: Perfect score: US-09-771-961-2 1709 .

Sequence: 1 MCSTSGCDLEEIPLDDDDLN......WIQQHGGWEKILGISHEEVD 327

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

rched: 105224 seqs, 38719550 residues

otal number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		29 88			88		24 89	89	89.	21 89.5		90.	9	17 91.5	9	92.	92.5	93	93	94.5	96	7	99	105.5	114	5 115	117		2 119	1 128.5	Result Qu No. Score Ma
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TDT_MONDO	BAXA_HUMAN	TEC1_YEAST	POLG_PYFV1	NOTC_XENLA			z	FA8_MOUSE	UVRG_DROME	BAXB_HUMAN	KAR1_YEAST	BAXA_RAT	ZIP1_YEAST	TDT_BOVIN	DPO1_BACSU	RPN2_YEAST	GGA3_HUMAN	PMS2_MOUSE	AR11_XENLA	BAXA_MOUSE	AKA6_HUMAN	SYK_AQUAE	YVDK_BACSU	SECA_HAEIN	BCLX_PIG	TDT_MOUSE	BCLX_HUMAN	BCLX_RAT	BCLX_MOUSE	BCLX_CHICK	ID
002789 monodelphis		saccharo	7 parsnip			P29375 homo sapien			_	-		_	saco	bos taur	-	sacc	homo	mus musc	xeno	3 mus m		00		3 haem	sus	n som 8	7	ratt	mus mu	6 gallus ga	Description

## ALIGNMENTS

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SEQUENCE FROM N.A. (LONG FORM). STRAIN-HUBBARD WHITE MOUNTAIN; TISSUE-Testis; WIDIFINE-97264485; PubMed-9110311; Vilagrasa X., Mezquita C., Mezquita J.; "Differential expression of bc1-2 and bc1-x during chicken spermatogenesis.", 47:26-29(1997).  ***Initial expression of bc1-2 and bc1-x during chicken spermatogenesis.", 47:26-29(1997).  ***Initial expression of bc1-2 and bc1-x during chicken spermatogenesis.", 47:26-29(1997).  ***Initial expression of bc1-2 and bc1-x during chicken spermatogenesis.", 47:26-29(1997).  ***Initial expression of bc1-2 and bc1-x during chicken spermatogenesis.", 47:26-29(1997).  ***Initial expression of bc1-2 and bc1-x during chicken spermatogenesis.", 47:26-29(1997).  ***Initial expression of bc1-2 initial periodic and periodic and initial expression in collaboration spermatogenesis.", 47:26-29(1997).  ***Initial expression of bc1-2 initial periodic and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	CHICK CHICK STANDARD; PRT; 229 AA.  COTRETC, COR8908;  01-FEB-1995 (Rel. 31, Created)  01-NOV-1997 (Rel. 35, Last sequence update)  16-OCT-2001 (Rel. 40, Last annotation update)  Apoptosis regulator Bc1-x.  BC12L1 OR BCLX OR BCL-x.  Gallus gallus (Chicken).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  Gallus.  Gallus.  Gallus.  Gallus.  Gallus.  SEQUENCE FROM N.A. (SHORT FORM).  MEDLINE-93364977; PubMed-8358789;  Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  Turka L.A., Mao X., Nunez G., Thompson C.B.;  "bc1-x, a bc1-2-related gene that functions as a dominant regulator of apoptotic cell death.";  Cell 74:597-608(1993).

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Best Local
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                                                                                                                                                                                                                                                                                          BCLX_MOUSE STANDARD; PRT; 233 AA. 064373; Q60657; Q60658; Q61338; Q613073; Q60657; Q60658; Q61338; Q61657; Q61657; Q61658; Q61338; Q61657; Q616573; Q616573;
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                              _MOUSE
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SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
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Pfam; PF00452; Bcl-2;
Pfam; PF02180; BH4; 1
                                      Gonzalez-Garcia M., Perez-Ballestero
                                                  SEQUENCE FROM N.A. (ISOFORMS X(L) STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=95331139; PubMed=7607090;
                                                                                                                                   STRAIN=2A4B;
Kamesaki H.,
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                Apoptosis regulator Bcl-x. BCL2L1 OR BCL2L OR BCLX. Mus musculus (Mouse).
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DOMAIN
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PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
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                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTAIDNHPMNRVLGFGTKYLKENFSPWIQQHGGWEKILGI 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TQAGGFKSKEIFVTEGLSFQLQGHV----PVASSSKKDEEEQILAKIVELLKYSGDQLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSNRELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSP----SWHPP--
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49; Conser
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125
176
206
185
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вн3;
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96
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22.3%;
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                                                                                                                   the
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                                                                                                                   Takatsu K., Okuma N
e EMBL/GenBank/DDBJ
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                                                                                    (L)
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ERFVDLYGNAAABELRKGQETFNKWLLTGATVAGVLLLGSL
LSRK -> VRTALP (IN SHORT ISOFORM).

A97D3A4D04C0E9DA CRC64;
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                                                                                     AND
                                      R.,
                                                                                     X(BETA))
                                                                                                                                    Okuma M
                                    Ding L.,
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                                                                                                                     databases
                                      Duan L.,
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                                      Boise L.H.,
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"bcl-XL is the major bcl-x mRNA form expressed during murine development and its product localizes to mitochondria."; Development 120:3033-3042(1994).
       EMBL;
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J. Immunol. 158:4750-4757(1997).
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MEDLINE=97289584; PubMed=9144489;
Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6 X CBA;
MEDLINE=98051053; Pub
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Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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"A novel Bcl-x isoform connected to the T cell receptor regulates
apoptosis in T cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bc12 family members and for repression of cell death. PTM: Proteclytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has protected activity (By similarity). CONTAINS 1 BC1-2 HOMOLOGY DOMAIN 1 (BH1). SIMILARITY: CONTAINS 1 BC1-2 HOMOLOGY DOMAIN 2 (BH2). SIMILARITY: CONTAINS 1 BC1-2 HOMOLOGY DOMAIN 3 (BH3). SIMILARITY: BELONGING TO THE BC1-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOFORM promotes apoptosis.

SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity).

SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).

ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCX-X(L) (SHOWN HERE), BCL-X(S),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLICING.
TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA BEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-x(S) isoform promotes appears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN POSTNATAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATED.
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   L35049;
L35048;
U10102;
U10101;
                                                                                                                                                       x83574;
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CAA58557.1; -.; AAA51039.1; -.; AAA51040.1; -.; AAA82174.1; -.; AAA82173.1; -.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORM X(BETA))
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σ10100; σ51279; U78031; U78030;

AAA82172.1; AAC53460.1;

AAB96881.1; -. AAB96881.1; JOINED.

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Best Local
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                                                                 BCLX_RAT STANDARD; PRT; 233 AA. P53563; Q62678; P70614; P70613; Q62836; Q64087; Q1-0CT-1996 (Rel. 34, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                            Apoptosis regulator Bcl-x. BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; BCL_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:88139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                     306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRANSMEN
                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                              131 SRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQL 190
                                                                                                                                                                                                                                                                                                                         58
                                                                                                                                                                                                                                                                                                                                                                                          77 SQSSEKAI-----NLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQW 130
                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                           ω
                                                                                                                                                                                                    SPWIQQHGGWEKILGI 321
                                                                                                                                                                                                                                                                                               QGHVPVASSSKKDEEEQI-LAKIVELLKYSGDQLE---RKLKKDKALMGHFQDGLSYSVF
                                                                                                                                                                                                                                                                                                                                                                      SQSNRELVVDFLSYKLSQKGYSWSQFSDVEENR----TEAPEETEAERETPSAINGNPSW 57
                                                                                                                                                                              EPWIQENGGWDTFVDL 194
                                                                                                                                                                                                                                                 KTITDQVLM-GVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFGTKYLKENF 305
                                                                                                                                                                                                                                                                                                                         EQVVNELFRDGVN--WGRIVAFFSFGGALCVESVDKEMQV---LVSRIASWMATYLNDHL
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS01080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
86
129
180
210
210
126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194
                                                                                                                                                                                                                                                                        -SSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
148
195
226
188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 119; DB 1
Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X(DELTA-TM))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM BCL-X(S)).
DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYGNNAAAESRKGQERFNRWFLIGMTVAGVVLLGSLFSRK-> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCL-X(BETA))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
         Sciurognathi; Muridae; Murinae;
                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24D2AC79887E072E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                    91;
                                                                                                                                                                                                                                                                                                                        ----NGAT---
                                                                                                        Q64128;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     74;
         Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                          123
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STRAIN-SPRACUE-DAWLEY; TISSUB-Ovary;
MEDLINE-95129487; PubMed-7828536;
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
"Expression of members of the bc1-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulos cell apoptosis is associated with decreased bax and constitutive bc1-2 and bc1-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol.
                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shiraiwa N., Inohara N., Okada S., Yuzaki M. "An additional form of rat Bcl-x, Bcl-xbeta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wesselingh S.L., David Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98010630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unspliced RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Thymus;
MEDLINE=96278736; PubMed=8662675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michaelidis T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morikawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aritomi M., Kunishima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                  The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                           SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT DETECTRALE LEVEL OF BCL-X(S).

DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimentration.
                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytochrome c, from the mitochondrial membrane. The Bc1-x($) are Bc1-x(beta) isoforms promote apoptosis.
SUBUNIT: Bc1-x(b) forms heterodimers with BAX, BAK and Bc1-2 (similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity).
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ELVELOPE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOL. Chem. 272:27886-27892(1997).
FUNCTION: Potent inhibitor of cell death. Inhibits activation caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to it and preventing the release of the caspase activator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structure of rat Bcl·xL. Implications for the function 2 protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promotes apoptosis in promyeloid 271:13258-13265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9346936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISOFORMS X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inohara N., Ishibashi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yuzaki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               generated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a M., Hard
databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell death by (VDAC) by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardwick J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bcl-x(S) and
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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RESULT 4
BCLX_HUMAN
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Best Local Similarity
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00337; BCL; 1.

SMART; SM00365; BH4; 1.

PROSITE; PS50062; BCL2_FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
Q07817; Q92976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
          BCLX_HUMAN
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                          171
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                                                                                                                                                           183
                                                                                                                                                                                                 123
                                                                                                                                        66
                                                                                                                                                                             54
                                                                                                                                                                                                                                        77
                                                         ATYLNDHLEPWIQENGGWDTFVDL 194
                                                                             TKYLKENFSPWIQQHGGWEKILGI 321
                                                                                                 PGTAYQSFEQVVNELFRDGVN--WGRIVAFFSFGGALCVESVDKEMQV---LVSRIASWM
                                                                                                                 DGLSYSVFKTITDQVLM-GVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFG 297
                                                                                                                                        - NGAT - - -
                                                                                                                                                          TEGLSFQLQGHVPVASSSKKDEEEQI-LAKIVELLKYSGDQLE---RKLKKDKALMGHFQ 238
                                                                                                                                                                             ----NPSW------HLADSPAV-----
                                                                                                                                                                                                 QDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIFV 182
                                                                                                                                                                                                                     SQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAING-----
                                                                                                                                                                                                                                       SQSSEKAI-----NLGKKKSSWKAFFGVVEK-----EDSQSTPAKVSAQGQRTLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1AF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X82537;
X82537;
U10579;
U72350;
U72349;
U34963;
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PF002180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S76513; AAC60701.1;
S78284; AAC60702.1;
                                                                                                                                                                                                                                                           54;
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IPR003093;
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64
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201
233
                                                                                                                                                                                                                                                           Conservative
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CAA57887.1;
AAA19257.1;
AAB17353.1;
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AAA77686.1;
           STANDARD;
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                                                                                                                                                                                                                                                                   6.9%;
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                                                                                                                                        SSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHIT
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                                                                                                                                                                                                                                                                                                            Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                    BH2.

POTENTIAL.

POTENTIAL.

MISSING (IN ISOFORM BCL-X(S)).

MISSING (IN ISOFORM BCL-X(BYTVAGVVLLGSL

FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED

IDVSGDIPGLL (IN ISOFORM BCL-X(BETA)).

R -> Q (IN REF. 1).

F -> S (IN REF. 2).

A -> E (IN REF. 2).

A -> U (IN REF. 4).

FF -> SS (IN REF. 4).

FF -> SS (IN REF. 4).
                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                           Score 118; DB Pred. No. 0.04; B; Mismatches
                                                                                                                                                                                                                                                                                                                     DD
           PRT;
                                                                                                                                                                                                                                                                                                                    v v
                                                                                                                                                                                                                                                                                                          2B62B6C63864BC8F CRC64;
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           233
           A
                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                           82;
                                                                                                                                                                                                                                                                            Length 233;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                      53
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Hardwick J.M.;
Hardwick J.M.;

"Modulation of cell death bx Bcl-xL through caspase interaction.";

Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).

-I- FUNCTION: Pottent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boise L.H., Gonzalez-Garcia M., Postema C.E. Turka L.A., Mao X., Nunez G., Thompson C.B., "bcl-x, a bcl-2-related gene that functions of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
Apoptosis regulator Bcl-x.
                                                                                                                                                                                                   MEDLINE=98118550; PubMed=9435230;
Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Ve
                                                                                                                                                                                                                                                                                           Ng S.L., Fesik S.W.;
"X-ray and NMR structure
cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng E.H.-Y., Levine B., Boise L.H., Korsmeyer S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95372373; PubMed=7644501; Sedlak T.W., Oltvai Z.N., Yang E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)). MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis regulator Bcl-BCL2L1 OR BCL2L OR BCLX.
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                                                                                                                                                                                                                                                  CLEAVAGE BY CASPASES, AND MUTAGENESIS
                                                                                                                                                                                                                                                                   Nature 381:335-341(1996).
[7]
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96256675; PubMed=8692274;
                                                                                                                                                                                                                                                                                                                                                                                                                           Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J., Thompson C.B., Fesik S.W.;
"Structure of Bcl.xL-Bak peptide complex: recognition between regulators of apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Korsmeyer S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM BETA). Inohara N., Ohta S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                         Yoon
                                                                                                                                                                                                                                                                                                                                                       Muchmore
                                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sattler M., Liang H., Nettesheim D., Meadows R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97172562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 1-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 379:554-556(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96170038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Froc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Multiple Bcl-2 family members demonstrate selective dimerizations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Bax-independent inhibition
             apoptotic activity. SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES
                                                        isoform promotes apoptosis.
SUBUNIT: Bcl-x(L) forms het
ENVELOPE (BY
                                          Heterodimerization with BAX
                                                                                                                                                                                                                                                                                                                                      more S.W., Sattler M., Lian
H.S., Nettesheim D., Chang
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                                                                                                                                                                                                                                                                                                                        Fesik S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF BH1 AND BH2 DOMAINS. 70038; PubMed=8596636;
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Chang B.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of apoptosis
                                                        heterodimers with
                                                                                                                                                                                                                                                                                                         human Bcl-xL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92:7834-7838(1995)
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                                          does
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                                                                                                                                                                                                                                                                                                                                    Meadows R.P., Ha
, Thompson C.B.,
                                          not
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                                          seem
                                                                                                                                                                                                                                                                                                         an inhibitor of programmed
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                                                        BAX,
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               AND PERINUCLEAR
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                                                        BAK and Bcl-2.
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DOMAIN 4 24 BH4.
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SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; BcL-2.
Pfam; PF00452; BcL-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
LYMPHOCYTES: IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.

DOMAIN: The BH4 domain is required for anti-apoptotic activity.
The BH1 and BH2 domains are required for both heterodimerization
with other Bcl2 family members and for repression of cell death.
PTM: Proteolytically cleaved by Caspases during apoptosis. The
cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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1LXL; 21-APR-97.
1MAZ; 21-APR-97.
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WD->GA: REDUCE
BY ABOUT HALF.
D->A: NO EFECT
G -> A (IN REF
                                                   D->A: NO
                                                                                                                                                                                         CLEAVAGE BY CASPASE-1.

MISSING (IN ISOFORM BCL-X(S)).

DTFVELYGNNAAAESKGQEEFURWFLITGMTVAGVVLLGSL
FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
VGDVDS (IN ISOFORM BCL-X(BETA)).
                                                                                                                                                      FRD->VRA:
                                                                                                                   GRI->ELN: LOSS OF ANTI-APOPTOTIC
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                                                                                                                                                                     CASPASE-3.
                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                ACTIVITY
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                         NO HETERODIMBERIZATION WITH BAX.
NO EFECT ON CASPASE-1 CLEAVAGE.
10 EFECT ON CASPASE-1 CLEAVAGE.
REDUCES ANTI-APOPTOTIC ACTIVIT
T HALF.
 NO EFECT ON CASPASE-1 CLEAVAGE (IN REF. 1; CAA80661).
                                                                                                                                                                                 CLEAVAGE
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                          Rougeon F., Doyen N.;
"The two isoforms of mouse terminal
                                                                                                                                                                                                                     Benedict C.L., Gilfillan S., Kearney J.F.;
"The long isoform of terminal deoxynucleotidyl transferase (TdtL)
enters the nucleus and, rather than cattalyzing N addition, modulates
the catalytic activity of the short isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doyen N., Fanton D'Andon M., Bentolila L.A., "Differential splicing in mouse thymus generaterminal deoxynucleotidyl transferase."; Nucleic Acids Res. 21:1187-1191(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=BALB/C; TIS MEDLINE=93219079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=86286588; PubMed=3755527;
Koiwai O., Yokota T., Kageyama T., Hirose T., Yoshida S., Arai K.;
"Isolation and characterization of bovine and mouse terminal deoxynucleotidyltransferase CDNAs expressible in mammalian cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                               Bentolila L.A., Fanton D'Andon M., Nguyen T.Q., Martinez
                                                                                                            PRELIMINARY CHARACTERIZATION OF ALTERNATIVE FORMS MEDLINE = 96016194; PubMed = 7556063;
                                                                                                                                                                                                 J. Exp. Med. 193:89-99(2001).
                                                                                                                                                                                                                                                                                                                                        PubMed=11136823;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIFV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQSSEKAI-----NLGKKKSSWKAFFGVVEK-----EDSQSTPAKVSAQGQRTLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGTAYQSFEQVVNELFRDGVN--WGRIVAFFSFGGALCVESVDKEMQV---LVSRIAAWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGLSYSVFKTITDQVLM-GVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NGAT----GH-----SSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NPSW------HLADSPAV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAING------
  in both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res. 14:5777-5792(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Thymus;
the ability to add N regions and subcellular
                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8464703;
                                                                                                                                                                                                                                                                                                                                                                                            (ISOFORMS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26049 MW;
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                                                                                                                                                                                                                                                                                                                                                                                         AND 2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E09D3CDD851AE9BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                             deoxynucleotidyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         generates
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.047;
                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nguyen T.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            two forms
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                                                                                                                                                                                                                                                                                                                                         Nuclear protein; /
DOMAIN 27
VARSPLIC 483
CONFLICT 26
CONFLICT 193
CONFLICT 193
CONFLICT 387
CONFLICT 387
CONFLICT 367
CONFLICT 441
CONFLICT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:98659; Dntt.
InterPro; IPR001357; BRCT.
InterPro; IPR002054; DNA_polx.
Pfam; PF00533; BRCT; 1.
Pfam; PF00966; DNA_polymerasex; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0869; DNAPOLX.

SMART; SM00292; BRCT; 1.

SMART; SM00483; POLXC; 1.

PROSITE; PSS0172; BRCT; 1.

PROSITE; PS00522; DNA_POLYMERASE_X; 1.

Transferase; Nucleotidyltransferase; Terminal addition; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; B23595; B23595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                       278
                                                                                                                               83
                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                 8 DLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS: 2 isoforms; TDT-L(arge)/TdtL (shown here) and TDT-S(mall)/TdtS; are produced by alternative splicing. The TDT-S form is the major form.

SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-X FAMILY.

SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulate the function of TdtS.

CATALYTIC ACTIVITY: N deoxynucleoside triphosphate + [deoxynucleotide](M) = N diphosphate + [deoxynucleotide](M+N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: TEMPLATE-INDEPENDENT DNA POLYMERASE WHICH CATALYZES THE RANDOM ADDITION OF DEOXYNUCLEOSIDE 5'-TRIPHOSPHATE TO THE 3'END OF A DNA INITIATOR. ONE OF THE IN-VIVO FUNCTION OF THIS ENZYME IS THE ADDITION OF WICLEOTIDES AT THE JUNCTION (N REGION) OF REARRANGED IG HEAVY CHAIN AND T CELL RECEPTOR GENE SEGMENTS DURING THE MATURATION OF B AND T CELLS. The Tdtl isoform seems to serve to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: REQUIRES MAGNESIUM.
                                                       QDSHSQQWSRC-----LSNVEQCLEHEAVDPKVISIANRVAEIVYSW-PPPQATQAGG 174
                       QSDKSLRFTQMQKAGFLYYEDLVSCVNR----PEAEAVSMLVKEAVVTFLPDALVTMTGG
                                                                                            SITEGITEDGESSEAKAVLNDERYKSFKLFTSVFGVGLK----TAEKWFRMGFRTLSKI
                                                                                                                           TEVSWPCRNSQSSE-KAINLGKKKSSWKAF---FGVVEKEDSQSTPAKVSAQGQRTL-EY 122
                                                                                                                                                                 DALDILAENDELRENEGSCLAFMRASSVLKSLPFPI-----TSMKDTEGI-PCLGDKVK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X04123; CAA27735.1; -. X68670; CAA48634.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF316014; AAK07884.1; -. AF316015; AAK07885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P06766; 1BPB.
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14:4221-4229(1995)
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative
                                                                                                                                                                                                                                                                                                                                                                 118
502
26
99
193
193
287
309
367
                                                                                                                                                                                                                                                      6.7%;
24.0%;
                                                                                                                                                                                                                                                                                                                              60331 MW;
                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM TDT-S).

T -> M (IN REF. 2).

L -> F (IN REF. 2).

R -> G (IN REF. 1).

Q -> K (IN REF. 1).

D -> H (IN REF. 1).

D -> H (IN REF. 1).

DRRA -> ECAC (IN REF. 1).

RAF -> AS (IN REF. 2).
                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                      Score 115; DB Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing.
                                                                                                                                                                                                                                                                                                                            NF -> AS (IN REF. 2).
E6B109DCF39C8107 CRC64;
                                                                                                                                                                                                                                      Mismatches 116;
                                                                                                                                                                                                                                                                     DB 1; Length 530;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                      16;
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RESULT

BULXA

DI BULXA

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TO TIS-J

DI 15-J

DI 18-O

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PROSITE; PS50062; B
PROSITE; PS01080; B
PROSITE; PS01258; B
PROSITE; PS01259; B
PROSITE; PS01260; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCLX_PIG
077737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression of apoptosis-associated genes in hibernating myocardium of pig."; Submitted (JAN-1998) to the EMBL/GanBank/none 2011.
                                                                                                                                                                                                                                                                                                             EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Apoptosis regulator Bcl-x.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                            Pfam; PF00452; BC1-2;
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig)
                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 KLKKDKA-----LMGHFQDGLSYSVFKTITDQVLMGVDPRGESEVKAQGFKAALV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity). Heterodimerization with BAX does not seem required for anti-apoptotic activity (By similarity). SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Potent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.

SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                          AJ001203;
Q07817; 1M
                                                                                                                                                                                                                                IPR003093;
IPR000712;
                                                                                                                                                                                                                                                                                   IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                        CAA04597.1; -.
                       BCL2_FAMILY; :
BH1; 1.
BH2; 1.
BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KMTGHDVDFLITSPEATEDEEQQLLHKVTDFWKQQGLLLYCDILES
                                                                                                                                                                                                                                Bcl_2.
                                                                                                                                                                                                                                                                BH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                         by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Darmer D.;
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in no way
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SECA_HAEIN
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                                                 SCIENCE 269:496-512(1995).

SCIENCE 269:496-512(1995).

SCIENCE IN COUPLING THE HYDROLYSIS OF ATP TO THE TRANSFER OF PRE-SECRETORY PERTPASMIC AND OUTER ATP TO THE TRANSFER OF PRE-SECRETORY PERTPASMIC AND OUTER MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).

-1- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
                                                                                                                                                                                                Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.F., Dougharty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fittchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                              STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350530; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECA OR HI0909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
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DOMAIN
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                                                                                                                                                                                        Venter J.C.;
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        SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF PLASMA MEMBRANE
                                         WHICH COMPRISE SECA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGHVPVASSSKKDEEEQI-LAKIVELLKYSGDQLE---RKLKKDKALMGHFQDGLSYSVF 246
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                        SIMILARITY
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233 AA;
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Pred. No. 0.08;
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                                       SECE, SECF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                  Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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NP_BIND 100 107

SEQUENCE 901 AA; 103
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        006993;
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Pfam; PF02810; SEC-C; 1.
Pfam; PF01043; SecA_protein;
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                                                                                                                                                                                                                                                                                                                                 Hypothetical
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                                                                                                                                                                                                                                              NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            766 LQTLDELWKEHLASMDYLRQGIHLRGYAQKDPKQEYKKESFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 YSVFKTI-----TDQVLMGVDPRG-----ESEVKAQGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 CLSNVEQCLEHEAVDPKVISIANRVAE-IVYSWPPPQA-TQAGGFKSKEIFVTEGLSFQL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 LNEGKLNLMRKAFTVAGEAMESKMLAKVIASAQAKVEAFHFDGRKNLLEYDDVANDQRHA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 INLGKKKSSWKAFFGVVEKEDSQ------STPAKVSA---QGQRT-LEYQDSHSQQWSR 132
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                                                                                                                                                                                                                                                                                                                                 transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Pred. No. 2;
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v; 2BD0190266BD77AE CRC64;
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Best Local :
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SYK_AQUAE
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z94043; CAB08040.1; -.
EMBL; Z99121; CAB15462.1; -.
SubtiList; BG12420; yvdK.
Hypothetical protein; Hydroli
SEQUENCE 757 AA; 88279 MW
                                                                                                                                                                                                                                                                                                                                                     Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 39, Last sequence update)
Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA LYSS OR AQ_1202.
                                                    InterPro;
                                                                                    EMBL; AE000728; AAC07218.1;
                                                                                                                                                                                                                                                                                                                   Nature 392:353-358(1998).
-I- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) =
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Aquificales; NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   067258;
                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 GNVANEDSNYQEQFWQEEAKG-----ADSHSGHLA-----AKTIENPFGTPRFTVLAA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 GVVEKEDS--QSTPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPK---VIS 152
                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CYtoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                   + L-lysyl-tRNA(Lys).
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKLGMKGALYPMVTFTGDECHNEWE----ITFEEI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKY-LKENESPWI-----QQHGGWEKILGISHEEV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDARLNIGPKGFTGEKYGGAAYWDTEAYAVPMYLATAEPEVTKNLLLYRYHQLEAAKRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKAKELLADVVENGYEDAKRRHTDRWKERWAKADIEIKGDEELQQGIRYNIFQLFSTYYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKIVELL------KYSGDQLERKLKKDKALMG--HFQDGLSYSVFKTIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANETEGFVHE-----SFKTTEMYVENRYSYQTKASLKKFVIVTTSRDFREEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IANRVAEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHVP---VASSSKKDEEEQIL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQVLMGVDPRGESEVKAQG------FKAALVIDVTAKLTAIDNHPMNRVLGFG
                                                                     P14825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                     IPR002106; AA_tRNA_ligase_II.
IPR002309; tRNA-synt_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; Hydrolase; Glycosidase; Complete proteome
88279 MW; 75B3ECE933850F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%;
21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligase) (LYSRS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKA6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKA6_HUMAN STANDARD; PRT; 2319 AA. Q13023; 015028; 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update)
                                                                                                                                Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-99343692; PubMed=10413680;

Kapiloff M.S., Shillace R.V., Westphal A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0982; TRNASYNTHLYS.

PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.

PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PRKA6) (A-Kinase anchor protein 100 kDa) (AKAP 100) (mAKAP). AKAP6 OR AKAP100 OR KIAA0311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 597 AA; 70024 MW; 66D6DAB0D588819B CRC64;
               MEDLINE=95238446; PubMed=7721854;
MCCartney S., Little B.M., Langeberg L.K., Scott J.D.;
"Cloning and characterization of A-kinase anchor protein 100
                                                TISSUE-Hippocampus;
MEDLINE-95238446; P
                                                                                                                                                                                                                                        TISSUE=Brain
                                                                                                                                                                                                                                                        SEQUENCE OF 934-2319 FROM N.A.
                                                                                                                                                                                                                                                                                                               "mAKAP: an A-kinase anchoring protein
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                    SEQUENCE OF 1666-2319 FROM N.A.
                                                                                                                                                                                                                       MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 GLKDVEVRYRQRYLDLIANPEARRIFMLRTKLITE-MRKFFEMHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                       differentiated myocytes.";
Cell Sci. 112:2725-2736(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFKAALVIDVTAKLTAIDNHPMNRVLGFGTKYLKENFSPWIQQHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVIGEEKLKFFNDYIDVGDIVGVRGKLFRTNTGELTVEVEEYQLLAKSLHPLPE----KWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVLTEEEGEEVYKIKEQFDYDPNFRPVSLAGRLVSMRSMGKAIFGHIQDLTGKIQIYLKK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGYMVRLADEKGIEI-----LVF-----TKEEGLKPKESYTFEGILKRVEGKLSLVE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHVPVAS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKAINLGKKKSSWKAFFGVVEKEDSQSTPA--KVSAQGQRTLEYQDSHSQQWSRCLSNVE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKGINPYPYRFEVTDFIGNIRKQYEEEPPENYKVRVKGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSKKDEEEQILAKIVELLKYS-----GDQLERKLKKDKALMGHFQD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00152; tRNA-synt_2; 1. PF01336; tRNA_anti; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 59; Conserv
                                                                                                                     4:141-150(1997).
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   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%;
20.7%;
targets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 97;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 5.3;
Mismatches 109;
                                                                                                                                                                                                                                                                                                                         targeted
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   to the
                                                                                                                                                                                                                                                                                                                                       Scott J.D.;
                                                                                                                                                      from brain which
                                                                                                                                                                                                                                                                                                                         to the
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   sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288
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                                                                                                                                                                                                                                                                                                                         nuclear membrane
                                                                                                                                                                        genes.
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Best Local
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           BAXA_MOUSE STANDARD; PRT; 192 AA (207813; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00435; spectrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB0023
MIM; 604691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U17195; AAA92354.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reticulum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002017; Spectrin
                                                                                                                                                                                 868
                                                                                                                                                                                                                                                                                                                                                                                                                                     77
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FUNCTION: BINDS TO TYPE II REGULATORY SUBUNITS OF PROTEIN KINASE AND ANCHORS/TARGETS THEM TO THE NUCLEAR MEMBRANE OR SARCOPLASMIC RETICULUM. MAY ACT AS AN ADAPTER FOR ASSEMBLING MULTIPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CALCINEURIN) AND AKAP79.
SUBCELLULAR LOCATION: SARCOPLASMIC RETICULUM AND NUCLEAR MEMBRANE IN HEART MUSCLE. PARTICIPATION OF MULTIPLE TARGETING SIGNALS ALLOW CORRECT INTRACELLULAR TARGETING. THESE MAY BE REPEATED MOTIFS RICH IN BASIC AND HYDROPHOBIC AMINO ACIDS, PALMITOYLATED/MYRISTOYLATED MOTIFS OR ALTERNATIVELY SPLICE TARGETING SEQUENCES.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN CARDIAC AND SKELETAL MUSCLE, FOLLOWED BY BRAIN.
DOMAIN: RII-ALPHA BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC DOMAIN: RII-ALPHA BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC HELIX, COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURFACE ON THE R-SUBUNIT DIMER.
SIMILARITY: CONTAINS 2 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: INTERACTS WITH RII SUBUNIT OF PKA, PHOSPHATASE 2B
                                                                                                                                                                                                                                                                                                                                                                                                                               SQSSEKAINLGKK------KSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQD 124
                                                                                                                                                                              WKELQRQIKRQHSWILRALDTIKAEILATDVSVEDEEGTG-SPKAEVQL
                                                                                                                                                                                                               ---LERKLKKDKALMGHFQDGLSYSVFKT---ITDQVLMGVDPRGESEV 265
                                                                                                                                                                                                                                                                                    QAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIV-----ELLKYSGDQ
                                                                                                                                                                                                                                                                                                                                                                                             SSSSDIASSLGESIESGPLSDILSDEESSMPLAGMKKYADEKSERASSS-----EKNE 751
                                                                                                                                                                                                                                                                                                                        SHSATKSALIQKLMQDIQHQDNYEAIWEKIEGFVNKLDEFIQWLNEAMETTENWTPPKAE 811
                                                                                                                                                                                                                                                                                                                                                          SHSQQWSRCLSNVEQCLEH----EAVDPKVISIANRVAEIVY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                     MDDLKLYLETHLSFKLNVDSHCALKEAVEEEGHQLLELIASHKAGLKDMLRMIASQ
 regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762
1036
1560
2063
974
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1150
1701
2076
974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECTRIN 1.

SPECTRIN 2.

SER-RICH.

SER-RICH.

SER-RICH.

SER-RICH.

SER-RICH.

SER-RICH.

PKA-RII SUBUNIT BINDING DOMAIN.

C -> W (IN REF. 2).

V -> A (IN REF. 2).

MW; 3D3037AE40FCCFEE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
isoform alpha
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                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Length 2319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and for
                                                                                                                                                                                                                                                                                                                                                            -SWPPPQAT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oltvai Z.N., Milliman C.L., Korsmeyer "Bc1-2 heterodimerizes in vivo with a accelerates programmed cell death."; Cell 74:609-619(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00452; Bcl-2; 1
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L22472; AAA03622.1; -.. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE=93364978; PubMed=8358790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01259; BH3; 1. PROSITE; PS50062; BCL2_FAMILY; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002475; BCL2_f
InterPro; IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:99702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis;
                                                                                                                                                                                  172 AGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQI-----
                                                         222 QLERKLKKDKALMGHFQDGLSYSVFKTITDQVLMGVDPRGESEVKAQGFKAALVID-VTA 280
                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND ANYAGONIZING THE APPOPOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG EIB 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE CESSATION OF SPERM PRODUCTION.
SUBUNIT: FORMS HOMOLIMERS AND HETERODIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
SUBCELLULAR LOCATION: Membrane-bound.
ALTERNATIVE PRODUCTS: A 21 KDA MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLICING.
ELDSNMELQRMIADVDTDSPREVFFRVAADMFADGNFNWGR-VVALFYFASKLVLKALCT
                                                                                                                         SGGPTSSEQIMKTG-AFLLQGFIQDRAGRMAGETPELTLEQPPQDASTKKLSECLRRIGD
                                                                                                                                                                                                                                               l Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                            150
172
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Alternative splicing
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bax.
                                                                                                                                                                                                                                                                                                                                                                                            118 BI
165 BI
192 PO
21394 MW;
                                                                                                                                                                                                                                                                         23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL2_family
                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                         Score 94.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                     D2E0B3566579FAFF CRC64;
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a conserved homolog, Bax, that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.J.;
                                                                                                                                                                                                                                                                                                         DВ
                                                                                                                                                                                                                                               77;
                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                  -LAKIVELLKYSGD
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                                                                                                                                                                                                                                               17;
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                                                                                                                                                                                                                                               Gaps
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Qy

281

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128 KVPEL----IRTIMGWTLDFLRERLLVWIQDQGGWEGIL 162

KLTAIDNHPMNRVLGFGTKYLKENFSPWIQQHGGWEKIL 319

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                                                                                                                                                                                                 SOSO
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
AR11_XENLA
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95331613; PubMed-7607538;

Cruz-Reyes J., Tata J.R.;
"Cloning, characterization and expression of two Xenopus bcl-2-like cell-survival genes.";

Gene 158:171-179(1995).

-i- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.

-i- SUBCELLULAR LOCATION: Membrane-bound (Potential).
                                                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                              Pfam; PF00452; Bc1-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eamphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last anotation update)
Apoptosis regulator R11 (XR11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR11_XENLA
Q91828;
                                                                                                                                                                                                                                                                              PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X82461; CAA57844.1; -. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro,
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
                  191
                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED. SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES
QGHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKLKKDKALMGHFQDGLSYSVFKTIT 250
                                               SKKLSQNEACRK-----FSNNPNPMPYLMEPSTSERPG------EGAT---
                                                                              SRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQL 190
                                                                                                                 43;
                                                                                                                                                                                                                              ; Transmembrane.
101 120
152 167
                                                                                                                                                                                                                                                                                                                                                                                               IPR000712; Bcl_2.
                                                                                                                                                                                                 204 AA;
                                                                                                                                                                                                                 181
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                 198
23379
                                                                                                                              5.4%;
                                                                                                                                                                                                 MW.
                                                                                                                                Score 93; DB Pred. No. 2.7;
                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                               3BFC6BE6DDA4CA03 CRC64;
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                               DB 1; Length 204;
                                                                                                                 58;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
; Pipidae;
                                                                                                                 74;
                                                                                                               Gaps
                                               50
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996
01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Warren G., Dilikay R.M.;
Flavell R.A., Liskay R.M.;
"Male mice defective in the DNA mismatch repair
"Male mice defective in the DNA mismatch repair
"Male mice defective in the DNA mismatch repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95354212; PubMed=7628019; Baker S.M., Bronner C.E., Zhang L., Warren G., Elliot E.A., Yu J., Ashl
                                                                                                                                                                                                                                                                       DNA repair.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002099; DNA_mis_repair.
InterPro; IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U28724; AAA87031.1; HSSP; P23367; 1BKN.
                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: PROBABLY INVOLVED IN THE REPAIR OF MISMATCHES IN DNA.
-i- SUBUNIT: HETERODIMER OF PMS2 AND MLH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 82:309-319(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMS1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P54279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMS2_MOUSE
                                                                                                                                                                                                                                                                                                     PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:104288; Pms2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090
                             164 WPPPQATQAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYSGDQL 223
                                                                                            112 VSAQGQRTLEYQDSHSQQWSRC-----LSNVEQCL--EHEAVDPKVISIANRVAEIVYS 163
                                                                                                                            463 ISYRGLRGSQDKLVSPTDSPGDCMDREKIEKDSGLSSTSAGSEEEFSTPEVASSFSSDYN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 IVQWMVNYLEHTLQPWMQENGGWEAFVGL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 VLGFGTKYLKENFSPWIQQHGGWEKILGI
                                                                                                                                                           53 LSQRGL-GNCSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
----SPTNAKRFKTEERPSNVNISQRLPG--PQSTSAAEVDVAIKMNKRIVLLEFSLSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALCVESANKEMTDL----LPR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQVLMGVDPRGESEVKAQG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGIV-----EEEVLQALLEATE----EFELRYQRA--
                                                              VSS----
                                                                                                                                                                                                                                                                                                                   PF01119; DNA_mis_repair; 1.
PF02518; HATPase_c; 1.
                                                                                                                                                                                           61;
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                        859 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 35, Last annotation update)
n homolog 2 (DNA mismatch repair p.
                                                                                                                                                                                           Conservative
                                                              -LEDRPSQETINCGDLDCRPPGTGQSLKPEDHGYQCKALPLARL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                        5.4%;
                                                                                                                                                                                                                                                                        95225 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu J., Ashley
                                                                                                                                                                                           46;
                                                                                                                                                                                                          Score 93; DB Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                        263B5A6BBBB2ACA9 CRC64;
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plug A.,
Ley T., Arr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arnheim
                                                                                                                                                                                                                        1;
                                                                                                                                                                                           124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robatzek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                                        Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene PMS2 exhibit
                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions on
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                                                                                                                                                                                           44;
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                                                                                                                                                                                         Gaps
                                                              568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96127530; PubMed-8590280;
MEDLINE-96127530; PubMed-8590280;
Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
"Prediction of the coding sequences of unidentified human genes.
The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced analysis of cDNA clones from human cell line KG-1.";
DNA Res. 2:167-174(1995).

THE REGULATION OF MEMBRANE TRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGA3_HUMAN STANDARD; PRT; 723 AA.
Q9NZ52; Q9UYX3; Q15017;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP-ribosylation factor binding protein GGA3 (Golgi-localized, gamma ear-containing, ARP-binding protein 3).
GGA3 OR KIAA0154.
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boman A.L., Zhang C.-J., Zhu X., Kahn R.A.;
"A family of ADP-ribosylation factor effectors that can transport through the trans-Golgi.";
Mol. Biol. Cell 11:1241-1255(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (SHORT ISOFORM). MEDLINE=20214818; PubMed=10749927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20211638; PubMed=10747089; Dell'Angelica E.C., Puertollano R.
          EMBL; AF190864; AAF05709.1; -.
EMBL; AF219139; AAF42849.1; -.
EMBL; D63876; BAA09926.1; ALT_INIT.
InterPro; IPR001121; G_adapt_C.
InterPro; IPR002014; HRS.
                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "GGAs: a family of ADP ribosylation factor-binding adaptors and associated with the Golgi complex."; J. Cell Biol. 149:81-94(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vargas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TRANS-GOLGI NETWORK.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HE SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 GAMMA-ADAPTIN C-TERMINAL DOMAIN.
SIMILARITY: CONTAINS 1 VHS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               THROUGH THE TRANS-GOLGI NETWORK. SUBUNIT: BINDS TO ARF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKRMKQLQHLKAQNKHELSYRKFRA---KICPGENQAAEDELRKEISKSMFAEMEILGQF 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERKLKKDKALMGHFQDGLSYSVFKTITDQVLMGVDPRGESEVKAQGFKAALV-IDVTAKL 282
                                                                                                            AF219138; AAF42848.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ngelica E.C., Puertollano R., Mullins C., Aguilar R.C
J.D., Hartnell L.M., Bonifacino J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LGFIVTKLKEDLF-LVDQHAADEK 703
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RPN2_YEAST
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Best Local S
Matches 65
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PROSITE; PS50179; VHS; 1.

PROTECH Transport; Golgi stack; Coiled coil; Alternative splicing.

DOMAIN 1 31 BINDS TO ARF1 (IN LONG ISOFORM).

DOMAIN 16 146 VHS.

DOMAIN 188 232 COILED COIL (POTENTIAL).

DOMAIN 357 360 POLY-PRO.

DOMAIN 453 457 POLY-SER.

DOMAIN 453 457 POLY-SER.

DOMAIN 624 629 POLY-VAL.

DOMAIN 598 709 GAMMA ADAPTIN C-TERMINAL.

DOMAIN 598 709 GAMMA ADAPTIN C-TERMINAL.

VARSPLIC 68 100 MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPN2_YEAST STANDARD; PRT; 945 AA. 932565; 01-OCT-1993 (Rel. 27, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD003686; HRS; 1.
ProDom; PD021457; G_adapt_C;
SMART; SM00288; VHS; 1.
PROSITE; PS50179; VHS; 1.
                                                                                                                                                                                                                                                  Demarini D.J., Papa F.R., Swaminathan S., Ursic D., Rasmussen Culbertson M.R., Hochstrasser M.; "The yeast SEN3 gene encodes a regulatory subunit of the 26S proteasome complex required for ubiquitin-dependent protein
            Gentles S.,
                                      STRAIN=S288C / AB972;
Barrell B.G., Badcock
Churcher C.M., Connor
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=96026012; PubMed=7565784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26S proteasome regulatory subunit RPN2.
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                            degradation in vivo.
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G., Badcock K., I
M., Connor R., (
Hamlyn N., Hors
                                                                                                                                                                                               Biol.
                                                                                                                                                                                            15:6311-6321(1995)
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         K., Bankier A.T., Bowman S., Brown D.,
R., Copsey T., Dear S., Devlin K., Fraser
Horsnell T.S., Hunt S., Jagels K., Jones
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EMBL; L06321; AAA87613.1; -.
PIR; S30804; S30804
PIR; S48369; S48369;
SGD; S0001337; RRN2.
InterPro; IPR002015; APC_proteasome.
Pfam; PF01851; PC_rep; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Louis E.J., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTS AS A REGULATORY SUBUNIT OF THE 26 PROTEASOME WHICH
IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S1 FAMILY.
-!- SIMILARITY: CONTAINS 10 PC REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteasome; Repeat.
                                                                                                                                                                                                                                                                                                                                                                     366 TATASLGVIHK 376
                                                                                                                                                                                                                                                      248 ENDEGLSAQIAFDLVSSASQQLLEILVTELTAQGYDPAL-LNILSGLPTCDYYNTFLLNN 306
                                                                                                                                                                                                                                                                                                                                    188 YLLTLAITTVTNSKFRSSILRKSFDFLMNMPNCDYLTLNKVVVNLNDAGLALQLFKKLKE 247
                                                                                                                                                                                                                                                                                                                                                                                                               307 KNIDIGLLNKSKSSLDGKFSLFHTAVSVANGFMHAGTTDNSFIKANL-PWLGKAQNWAKF 365
                                                                                                                                                                                                                  292 RVLGFG-----
                                                                                                                                                                                                                                                                                             252 QVLMGVDPRGE-----N 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 YSWPPPQATQAGGFKSKEIFVTEGLSFQLQGH----VPVASSSKKDEE---EQILAKIVE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 EDSQSTPAKVSAQGQRTLE-YQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 FDIDEKSQFVETIVSKSIEMYVQEASKQYTK----DEQFYTKDIIDPKLTSIFERMIEKC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 NCSANESWTEVSWPCRNSQ--------SSEKAINLGKKKSSWKAFFGVVEK 102
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                                                                                                                                      -----LGISHE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNVVDQLWSEISNELPDIEALYDDDTFSDREMAALIASKVYYNLGEYESAVKYALAAKDR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
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945 AA; 104231 MW; 881E78EBC6BD934F CRC64;
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                    2002, 16:40:06
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                                                                                                                                                                                                              --TKYLKENFSPWIQQHGGWEKI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 129; Gaps
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Title: US-09-771-961-2
Perfect score: 1709
Sequence: \ 1 MCSTSGCDLEEIPLDDDDLN......WIQQHGGWEKILGISHEEVD 327
                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                        Scoring table:
otal number of hits satisfying chosen parameters:
                                                       rched:
                                                                                                                                                                                                                                                      June 19, 2002, 16:32:27 ; Search time 31.42 Seconds (without alignments) 1000.039 Million cell updates/sec
                                                283138 seqs, 96089334 residues
                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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       283138
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	5	4	ω	N	1		No.	5 2 1 +
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547	1384	1083	880	333	945	670	450	1123	561	192	699	1055	597	462	757	2052	414	901	529	1647	562	227	233	214	233	233	190	233		Length I	
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A23595	T52301	T00790	E69680	T04656	S48369	F84540	T37702	A72311	T22917	D47538	AC0504	AD2499	G70403	G95233	C70034	C97038	A29835	H64101	B23595	T49412	T49904	JE0203	B47537	I49057	167431	I49056	A47537	S51761		ID	
	GYMNOS/PICKLE prot	fi	DNA polymerase I p	hypothetical prote	3	•	al prot	conserved hypothet	ന	bcl-2-associated p	ď	hypothetical prote	۳.	Cof family protein	othe	$\mathbf{o}$	SalI protein - Esc	preprotein translo	Q.		()		apoptosis regulato	transme	-Long -	Q.	ulat	tein -		Description	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	3	30
88.5	88.5	88.5	88.5	88.5	89	68	89	89.5	89.5	89.5	90	90.5	90.5	91	91
5.2	5. 2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5. 3	5.3	ა ა	υ ω	5.3
1447	1359	1333	578	445	2253	1722	926	2319	1029	218	433	878	472	1660	875
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T00530	B84645	E84601	D90564	B40590	T30336	I78879	E64171	A47004	F86210	B47538	S63143	A83748	A99098	A84647	S70115
	hypothetical prote	probable retroelem	hypothetical prote	flagellar distal c	nuclear/mitotic ap	retinoblastoma bin	hypothetical prote	coagulation factor	hypothetical prote	bcl-2-associated p	cell division cont	endo-beta-N-acetyl	conserved hypothet	ğ	ZIP1 protein - yea

## ALIGNMENTS

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apoptosis regulator bc1-x - chicken C; Species: Gallus gallus (chicken) C; Species: Gallus gallus (chicken) C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999 C; Accession: A47537 A; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L. Cell 74, 597-608, 1993 A; Title: bc1-x, a bc1-2-related gene that functions as a dominant regulator of apopt A; Reference number: A47537; MUID:93364977 A; Scatus: preliminary A; Accession: A47537 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-190 <BOI> A; Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899 C; Superfamily: bc1 transforming protein
                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mrNA
A;Residues: 1-233 <RES>
A;Cross-references: EMBL:U10101; NID:9506647; PIDN:AAA82173.1;
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
Submitted to the EMBL Data Library, November 1994
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an in
A;Reference number: $52866
A;Accession: $52866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bcl-x long - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: 149056; S52866
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
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C; Superfamily:
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A; Residues: 1-233 <KAM>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
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                                    SQSNRELVVDFLSYKLSQKGYSWSQFSDVEENR----TEAPEETEAERETPSAINGNPSW 57
                                                                                     SQSSEKAI-----NLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQW 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMRV---LVGRIVSWMTTYLTDHLDPWIQENGGW 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTAIDNHPMNRVLGFGTKYLKENFSPWIQQHGGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                             Similarity
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                                                                                                                                                          7.0%; Score 119; DB 2;
21.1%; Pred. No. 0.059;
                                                                                                                                      37;
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                                                                                                                                      Mismatches
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                                                                                                                                        91;
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A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487 A;Accession: I67431 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ
bcl-x transmembrane deleted - mouse C;Species: Mus musculus (bouse mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999 C;Accession: 149057 R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T ly A;Accession: 149057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004377 C;Superfamily: bcl transforming protein
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26
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A; Residues: 1-233 < RES>
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Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLSYSVFKTITDQVLM-GVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFGT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NGAT----GH----SSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 119; DB 2; Length 233; Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.; Cell 74, 597-608, 1993
Gell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic A;Reference number: A47537; MUID:93364977
Ccesssion: B47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis regulator bcl-xL - human
N;Alternate names: bcl-2-related protein
N;Contains: apoptosis regulator bcl-xS
C:Species: Homo sapiens (man)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: B47537; C47537
                                                                                                                                                                                      C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bc1-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bc1-xS #status predicts
    밁
                                           Q
                                                                                                                                                                                                                                                             A:Cross-references: GDB:228079
C:Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-69,'G',71-125,189-233 <BO2>
A; Cross-references: GB:L20122; NID:g623236;
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A:Gene: bcl-x-long
C:Gunerfamily: bcl transforming
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A;Molecule type: mRNA
A:Residues: 1-214 <RES>
                                                                                                                                                                                                                                                                                                           A; Gene: GDB: BCL2L
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L20121; NID:g510900; A;Accession: C47537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   latus: nucleic acid sequence not shown; translated oblecule type: mRNA; Residues: 1-233 <BOI>
                                                                                                                                                                                                                                                                                                                                 Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 QGHVPVASSSKKDEEEQI-LAKIVELLKYSGDQLE---RKLKKDKALMGHFQDGLSYSVF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
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                                           SQSSEKAI-----NLGKKKSSWKAFFGVVEK-----EDSQSTPAKVSAQGQRTLEY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWIQQHGGWE 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTITDQVLM-GVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFGTKYLKENF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQSNRELVVDFLSYKLSQKGYSWSQFSDVEENR----TEAPEETEAERETPSAINGNPSW 57
SQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAING-----
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                                                                                                             6.8%;
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21.5%; Pred. No. 0.063;
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                                                                                                           Score 117; DB 2
Pred. No. 0.085;
                                                                                    Mismatches
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                                                                                                                             DB 2;
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                                                                                    Gaps
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A;Cross-references: GB:U72398; NID:g162;
C;Genetics:
A;Gene: bcl-x
A;Map position: 20
C;Superfamily: bcl transforming protein
                                                                    hypothetical protein T24H18.70 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #t. C;Accession: T49904 R;Bevan, M.; Robben, J.; Grymonprez, B.; Volckaert, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N,Alternate names: h-bcl-xbeta (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 11-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999 (Spacession: JE0203 #S;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E. Biochem. Biophys. Res. Commun. 248, 147-152, 1998 #S;Title: Identification of a human CDNA encoding a novel bcl-x isoform.
submitted to the Protein S A; Reference number: Z25024 A; Accession: T49904
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A; Residues: 1-227 <BAN>
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                                                                                                                                                                                                                                                                                             171 ATYLNDHLEPWIQENGGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 TEGLSFQLQGHVPVASSSKKDEEEQI-LAKIVELLKYSGDQLE----RKLKKDKALMGHFQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 QDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIFV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 ATYLNDHLEPWIQENGGWD 189
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                                                                                                                                                                                                                                                                                                                                           298 TKYLKENFSPWIQQHGGW 315
                                                                                                                                                                                                                                                                                                                                                                                                                                         239 DGLSYSVFKTITDQVLM-GVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 ----NPSW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 SQSSEKAI-----NLGKKKSSWKAFFGVVEK------EDSQSTPAKVSAQGQRTLEY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAING-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                             Robben, J.; Grymonprez, B.; Volckaert, G.; the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHIT 115
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                                                                         Bancroft,
                                                                       Ι.;
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                                                                         Mewes,
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δõ
                                     В
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A;Molecule type: DNA
A;Molecule: 1-1647 <SCH>
A;Residues: 1-1647 <SCH>
A;Cross-references: EMBL:AL355928; GSPDB:GN00116; NCSP:B1D4.270
A;Cross-references: BAC clone B1D4; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
T49412
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A; Molecule type: DNA
A; Residues: 1-562 <BEV>
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                                                                                          Query Match
Best Local Similarity
Thes 71; Conserv
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                                                                                                                                                                                                    A;Gene: NCSP:B1D4.270
A;Map position: 6
                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein B1D4.270 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Decies: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 ccssion: T49412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AL353013; GSPDB:GN00063; ATSP:T24H18.70
A;Experimental source: cultivar Columbia; BAC clone T24H18
                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z25022
A;Accession: T49412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: ATSP:T24H18.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   hulte, U.; Aign, V.; Hoheisel, J.; Brand
nitted to the Protein Sequence Database,
                                     422
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118 -- RTLEYQDSHSQQWSRCLSNVEQCLEHE---
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                                                                       77
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                                     SPDSEAKVELGQDHVEGERKKESVAEAVVGLAEQADREAQEALARAEGQSAQAGITQDLE 481
                                                                    SQSSEKAINLG------KKKSSWKAFFGVVEKEDSQSTPAKVSAQGQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PWIQQ 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDRQANFSSF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QILAKIVELLKYSGDQLERKLKKDKALMGHFQDGLSYSVFKTITDQVLMG-----VDPR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWPPPQATQAG---GFKSKEIFVTEGLSFQLQGHVPVASS-----SKKDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVEKLKRELMEANRSRDAALTQVSEMKSSLGELSEKLQYLESYCDNLKKALREATEVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGQRTLEYQ-----DSHSQQWSRCLSNVEQCLEH----EAVDPKVISIANRVAEIVY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PLTDSHSAVVSSQPRNRGGRVMSWLFPKLKKKQKSNSIFNSPSITEKSEEVSEVLKDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPCRNSQS---SEKAINLG------KKKSSWKAFF---GVVEKEDSQSTPAKVSA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRHHVFKSTPALFSPKL------LRTRSLS-----QRGLGNCSANESWTEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SQENSGGRSSGKKNSEMPVSE--EVMVEGFLQIVSEARLSIKQFLKTLVSEIDEED
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                                                                                                                       6.6%;
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21.7%;
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                                                                                                                         Score 113.5;
Pred. No. 2.3;
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                                                                                                           Mismatches
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base, May 2000
-- AVDPKVISIANRVAEIVYSWPPP 167
                                                                                                                                             DB 2;
                                                                                                           102;
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                                                                                                          Gaps
                                                                       117
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-25, 'M', 27-98, 'F', 100-192, 'R', 194-286, 'Q', 288-308, 'E', 310-366, 'D', 368-44
A; Cross-references: EMBL: X68670; NID: 9287808; PIDN: CAA48634.1; PID: 9287809
C; Superfamily: DNA nucleotidylexotransferase
C; Keywords: alternative splicing; magnesium; nucleotidyltransferase; nucleus
                                                                                                                                                                                            A;Cross-references: GB:X04123; NID:g54765; PIDN:CAA27735.1; PID:g54766 R;Doyen, N.; d'Andon, M.F.; Bentolila, L.A.; Nguyen, Q.T.; Rougeon, F. Nuccleic Acids Res. 21, 1187-1191, 1993 A;Title: Differential splicing in mouse thymus generates two forms of the A;Reference number: $30235; MUID:93219079 A;A;Cossion: $30235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: B23595; S30235
R;Koiwall O.; Yokota, T.; Kageyama, T.; Hirose, T.; Yoshida, S.; Arai, K.
Nucleic Acids Res. 14, 5777-5792, 1986
A;Title: Isolation and characterization of bovine and mouse terminal deoxynucleotidyl
A;Reference number: A93633; MUID:86286588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA nucleotidylexotransferase (EC 2.7.7.31) - mouse N;Alternate names: terminal addition enzyme; terminal deoxyribonucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-529 <KOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B23595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LVSASESYMAYGMSKAGGLRVIRQEDGKDAKLF 644
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B δã Вþ Š 뫄 ρy Вþ β ρ В Matches Query Match Best Local Similarity 384 278 123 170 œ TFEKFKQPSRKVDALDHFQK--CFLILK--LDHGRVHSEKSGQQEGK--GWKAIRV 433 KLKKDKA------LMGHFQDGLSYSVFKTTTDQVLMGVDPRGESEVKAQGFKAALV 275 DALDILAENDELRENEGSCLAFMGASSVLKSLPFPI----TSMKDTEGI-PCLGDKVK 22 DLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESW 67 SIIEGIIEDGESSEAKAVLNDERYKSFKLFTSVFGVGLK-----TAEKWFRMGFRTLSKI 277 TEVSWPCRNSQSSE-KAINLGKKKSSWKAF---FGVVEKEDSQSTPAKVSAQGQRTL-EY 122 QSDKSLRFTKMQKAGFLYYEDLVSCVNR----PEAQAVSMLVKEAVVTFLPDALVTMTGG QDSHSQQWSRC-----LSNVEQCLEHEAVDPKVISIANRVAEIVYSW-PPPQATQAGG FKSKEIFVTEGLSFQLQGH----VPVASSSKKDEEEQILAKIVELLKYSG-----DQLER 225 Conservative -KMTGHDVDFLITSPEATEDEEQQLLHKVTHFWKQQGLLLYCDILES 6.6%; 24.0%; 48; Mismatches Score 113; DB 2; Pred. No. 0.53; 117; Length 529 Indels 60; Gaps 174 333 383 16;

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C;Accession: H64101
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preprotein translocase secA - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: preprotein translocase subunit
C;Species: Haemophilus influenzae
                                                                                                                                                                                                                       R;Finlay, B.B.; Paranchych, W.
J. Bacteriol. 166, 713-721, 1866
A;Title: Nucleotide sequence of the surface exclusion genes traS and traT from the A;Reference number: A29835; MUID:86223783
A;Accession: A29835
                                                                                                                                                                                                                                                                                                                                       C;Species: Escherichia coli
C;Date: 04-Aug-1988 #sequence_revision
C;Accession: A29835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630
A;Accession: H64101
                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-414 <FIN>
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                                                                                                                                                                                                    A; Status: preliminary
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Residues: 1-901 <TIGR>
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Best Local :
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                       Query Match
Best Local Similarity
                                                                                                                                         Genetics:
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 QGHVPVASSSKKD---EEEQILAKIVELLKYSGDQLERKLKKDKALMG-----HFQDGLS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 CLSNVEQCLEHEAVDPKVISIANRVAE-IVYSWPPPQA-TQAGGFKSKEIFVTEGLSFQL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657 IYEQRNHLLDNDDISETINAIRHDVFNGVIDQYIPPQSLEEQWDIKGLE----ERLSQEF 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              766 LQTLDELWKEHLASMDYLRQGIHLRGYAQKDPKQEYKKESFR 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 YSVFKTI-----TDQVLMGVDPRG-----ESEVKAQGFK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 INLGKKKSSWKAFFGVVEKEDSQ-----STPAKVSA---QGQRT-LEYQDSHSQQWSR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMELPISNWLEEDNNLHEESLRERIVEI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNEGKLNLMRKAFTVAGEAMESKMLAKVIASAQAKVEAFHFDGRKNLLEYDDVANDQRHA 656
                                                                                                               plasmid
  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli plasmid pED208 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Conservative
                       6.1%;
23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
  38;
                       Score 104; DB Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105.5; 1
Pred. No. 4.3;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                   04-Aug-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AEKEYKEKEALVGEDAMRHFEKGVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
  118;
                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
#status
                                               Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 901;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                                                                                                                                   23-Mar-1993
  38;
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
  10;
                                                                                                                                                                                                                                                                              IncF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
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                                                                                                             Q
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                                                                                                                                                                                                                                                                                            Qy
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, ; Daly, M.J.; Bennett, G.N.; Roonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacter, Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phage-related protein, YqbO B. subtilis homolog [imported] - Clostridium acetobutylic
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C97038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: CAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2052 <KUR>
                                                                                                                    В
                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001437; PIDN:AAK79094.1; A;Experimental source: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                                                                                                                                                                                                        437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 LTQQGGTSKGFSAQELKDFRDAMDVVTSSRVTDSGSHTDNASASLANQ-LSSTFSSLKSQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 -EHEAVDPKVISIANRVAEIVYSWPPPQAT-----QAGGFKSKEIFVTEGLSFQLQGHV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259
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539 DKFGDNTTQSNSILDALGGTMRKDWIDVLAK 569
                                                        258 DPRGESEVKAQGFKAAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAC1120
                                                                                                                                                                                                                                        WNKTADISMAKTADFAQVTDKAGMTSKDM----GISLNQLNGITAVLADNTGKSGNE----
                                                                                                                                                                                                                                                                                                ANRVAEIVYSWPP--PQATQAGGFKSKEIFVTEGLSF-QLQGHVPV-ASSSKKDEEEQIL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTGEIRNAISTNTEYEKNLVDLGRVLDSNKKSLQDFGQYAVRTSKEFGQDLGGIQSAMSS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKEYTQIQANSSAYLKLSESISQISSKSSLAMGSGNANNTFLDRMKISAAYAGSAVVIAS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGGWEKILGISHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVASSSKKDEEEQILAKIVELL---KYSGDQLERKLKKDKALMGHFQDGLSYSVFKTITD 251
                                                                                                                                                                            AKIVELLKYSGDQLER---
                                                                                                                                                                                                                                                                                                                                                            LAAQGVSAKKDLESMTKTVSL-GLNTSEITNS-NEMVQLLVSSMKQLGINFSDSEKVLDS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSDASASSNLTKALNTIQSIGSRYARDENTTLAEGIRAAATKSQDMSFGAGAS--VQGSV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IALGKTASSSWQQ-----QQRDALSEAQSLSNSLSQTSSLATSQMSQWSQQRGNSDTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                 KAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSWPCRNSQSS----EKAINLGK----KKS----
                                                                                                                    --IGDALKSMENRLERPKTLETLRGYGIEVMKDK---DHFKD-----FGDIVKEVSSAL 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Similarity
| 77; | Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DSDRQILGKVAGLVTGGKVSG---EAHLKGE----YTGRSGSSHGTSSD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%; Score 100; D
23.3%; Pred. No. 35;
                                                           --VIDVTAK 281
                                                                                                                                                                            ----KLKKDKALMGHFQDGLSYSVFKTITDQVLMGV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SW 93
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A; Experimental source: strain TIGR4 C; Genetics: A; Gene: SP1997

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C.Species: Bacillus subtilis
C.Species: Policy Secues
C.Species: Bacillus subtilis
C.Species: Policy Secues
C.Speci
                                                    R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heicon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95233
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COf family protein [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: G95233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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A;Cross-references: GB:AE005672; PIDN:AAK76064.1; PID:g14973505; GSPDB:GN00164;
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 AKLGMKGALYPMVTFTGDECHNEWE----ITFEEI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 TKY-LKENFSPWI-----QQHGGWEKILGISHEEV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 SKAKELLADVVENGYEDAKRRHTDRWKERWAKADIEIKGDEELQQGIRYNIFQLFSTYYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 AKIVELL------KYSGDQLERKLKKDKALMG--HFQDGLSYSVFKTIT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 DQVLMGVDPRGESEVKAQG------FKAALVIDVTAKLTAIDNHPMNRVLGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 MANETEGFVHE-----SFKTTEMYVENRYSYQTKASLKKFVIVTTSRDFREEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 GVVEKEDS--QSTPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPK---VIS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 5.8%; Score 99; DB 2; Length 757; Similarity 21.1%; Pred. No. 11;
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     TIGR:SP4
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Matches 48
                                                                        346 AVSQLHQALDKAADKVAKKTPAQQDLIGQV-DALIDTLYFTYGSFYLMGVDPERIFDIVH 404
                                                                                                                                                                                                                                                                        107 STPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHEAV--DPKVI------ 151
                                                                                                                                                      299 HHMMDERTQEEPRAWDLEGATHRAGFKIEELVEFVR------AASPSEEDFGQ 345
                                                                                                                                                                                            152 --SIANRVAEIVYSWPPPQATQAGGFKSKEI--FVTEGLSFQLQGHVPVASSSKKDEEEQ 207
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                                                                                                               ILAKIVELLKYSGDQLERKLKKDKALMGHFQDGLSYSVFKTITDQVLMGVDPRGESEVKA 267
QANMGKIFPDGKAHFDPVTHKILKPDN 431
                                     QGFKAALVID-----VTAKLTAIDN 287
                                                                                                                                                                                                                                                                                                                    1 Similarity
48; Conserv
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Search completed: June 19, 2002, 16:33:40 Job time: 73 sec

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match
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759
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HA10713 BM433532 BB576539 AQ884233 AA492696 BB589687	AI606692 AW000827	AA400686 BB746476	AW428115 BI360692	BB013694 AW484860	BI652080 AW414655	AA061006 AI614194	BF149673 BG895661	AW631581 BB615307	BF139422 BI342342	BB628327	BG176106	BF584699
BM433523 10m16H02 BM433523 10m16H02 BB576539 BB576539 AQ884233 HS_5504_B AA492696 v177e07.r BB589687 BB589687	wu45d10.		AW428115 64957 MAR BI360692 388694 MA	BB013694 BB013694 AW484860 62957 MAR	BI652080 603298866 AW414655 48366 MAR	AA061006 m146f07.r AI614194 vi77e07.y	BF149673 uy67g01.y BG895661 359228 MA	AW631581 90021 MAR BB615307 BB615307	$\sim$	œ	σ	BF584699 602098438

# ALIGNMENTS

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	source	FEATURES						COMMENT	JOURNAL	TITLE	REFERENCE	Olyonia torr	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	BI833102
/organ.sm="Homo saptens" /db_xref="taxon:9606" /clone="IMAGE:5229819" /clone=lib="NHI_MGC_120" /lab_host="DH10B" /lab_host="DH10B" /note="Organ: pooled pancreas and spleen; Vector: /note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is		High quality sequence stop: 803.  High quality sequence stop: 803.	gov	DNA sequencing by: Incyte Genomics, inc. Clone distribution: MGC clone distribution information can be	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	Tissue Procurement: Life Technologies, Inc.	Email: cgapbs-r@mail.nih.gov	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	1 (bases 1 to 980)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	numan.	ESG).	BI833102.1 GI:15944652	BI833102	mRNA sequence.	BI833102 980 bp mRNA linear EST 04-OCT-2001	

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                                                                            mRNA sequence.
BG718587
BG718587.1 GI:13997774
                                                                                                                BG718587 763 bp mkna ille
602696672F1 NIH_MGC_97 Homo sapiens cDNA clone
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 763)
                                       Homo sapiens
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237 c 244 g 217 t
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gtttattcctggccaccaccaccagggacccaggcaggaggcttcaagtccaaagagatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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National Institutes of Health, Mammalian Gene
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185 c 194 g 160 t
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/clone="IMAGE:4829032"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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                                                          ACCATAGAATTCAAAATCCTCGCCTACTACACCAGACATCATGTCTTCAAGAGCACCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llni.gov
Plate: LLAM10736 row: m column: 17
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National Institutes of Health, Mammalian
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KEYWORDS SOURCE FEATURES COMMENT REFERENCE VERSION ACCESSION DEFINITION TITLE AUTHORS ORGANISM JOURNAL source CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAMI1560 row: 1 column: 20 NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Unpublished (1999) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 715) Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, 603083677F1 High quality sequence stop: 715. Contact: Robert Strausberg, Ph.D. Homo sapiens BI838169.1 GI:15949719 mRNA sequence. /organism="Homo sapiens"
/db\_xref="taxon:9506"
/clone="IMAGE:522875"
/clone\_lib="NIH\_MGC\_120"
/lab\_host="DH10B" Location/Qualifiers NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5222875 5', 715 bp mRNA Inc Gene Collection (MGC) linear EST 04-OCT-2001

/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed);
source anonymous pool of spleen and pancreas from 28;

Library is oligo-dT primed and directionally cloned

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REFERENCE
AUTHORS
TITLE
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (Collection)
               Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NF Toshiyuki and Piero Carninoi (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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09; Conservative
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Contact: Robert Strausberg, Ph.D.
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BG717835.1 GI:13997022
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                                                                                       Email: cgapbs-r@mail.nih.gov
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Location/Qualifiers
                                         BI908814
603066277F1 NIH_MGC_118
BI908814
BI908814.1
                             mRNA sequence.
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/clone="IMAGE:4826292"
/clone_11b="NIH_MGC_97"
/lab_host="DH10B"
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 GI:16171889
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99.2%;
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Pred. No. 1.8e-133;
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                gttggaataccaagattcgcacagc-cagcagtggtccaggtgtctttctaa-cgtggag
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GTTGGAATACCAAGATTCGCACAGCGCAGCAGTGGTCCAGGTGTCTTTCTAAGCGTGGAG
                                                                             GTGGAGAAGGAAGATTCGCCAGAGCACGCCTGCCAAGGTCTCTGCTCAGGGTCAAAGGAC
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plate: LLAM11540 row: j column: 19
High quality sequence stop: 701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size 1.7 kb, insert size range full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5215218"
/clone_lib="NIH_MGC_118"
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/lab_host="DH10B"
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98.3%;
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                                     248
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aattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccctgctctct 127
                                                                                  caaatgagtcatggacagaggtgtcatggccttgcagaaattcccaatccagtgagaagg 247
                                                                                                                                                                                                        ATTTCAAAATCCTCGCCTACTACACCAGACATGATGTCTTCAAGAGCACCCCTGCTCTCT 95
                                                                     CATATGAGTCATGGACAGAGGTGTCATGGCCTTGCAGAAATTCCCCAATCCAGTGAGAAGG
                                                                                                                                      TCTCACCATAGCTGCTGAGAACAAGAAGTTTGTCCCACAGGGGCCTGCGGAATTGTTCAG 155
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keler,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
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HS_3049_Al_D07_MR CIT Approved Human Genomic Sperm Library E
Sapiens genomic clone Plate=3049 Col=13 Row=G, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3049 row: G column: 13
Class: BAC ends
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Fax: (206) 616-3887
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E-Coli DH10B"
a 101 c 104 g 105 t 2 others
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/db_xref="taxon:9606"
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2t60c07.rl Soares_testis_NHT Homo
5', mRNA sequence
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WashU_Merck EST_Project 1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov) fo
Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 406)
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                                                                                                                                                                                                                     (Pharmacia), digested with Not I and cloned into the and Eco RI sites of the modified pT7T3 vector. Libra went through one round of normalization to Cot5, an constructed by Bento Soares and M. Fatima Bonaldo.

101 g 82 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:726732"
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                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
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Functional annous.

Functional annous.

Nature 409, 685-690 (2001)

5 (bases I to 1535)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Av., Alaxawa, T., Bono, H., Brownstein, M., Bult, v., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Hanagaki, T., Arakawa, T., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hori, F., A., Hanagaki, T., Hori, F., Itoh, M., Izawa, M., Kasukawa, T.
                                                                                                                                                                                                                                                                                                                                                                                                                Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Haradda,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Genome Res. 10 (10), 1617-1630 (2000)
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Eutheria;
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                                                                                                                                                                                                                                                                                                                Exploration Research Group Phase
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Rodentia;
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mouse cDNA library
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                          accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct 120
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ATGTGCAGCACCAGTGTGTATGACCTGGAAGACATTCCCCTGGAGGATGATGATCCAAAC
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Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with BamHI and XhoI. cDNA of size comprised between 0.5 and 3 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall 3' end: BamHI. Host: DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details.
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                       /translation="MCSTSVYDLEDIPLEDDDPNSIEFKILAFYARHHVFKNTPAVFS PKLSRTRSLSQKALGTWSTDSWTQVSLPCRGSPSSEKNISJKKKSSWRTLFRVAEKE EGLESSPKEIRAQGPQGPFPVERQSGFNQHWPRSLSSYVEQRLESEPVDSKYAFIANR VAEIVYSWPPPDVIHSQGGSKLKERVSEILYFRFEGPCDSKNKDGEDQIISKIVELLK FSGDQLGREIKKDRALMSSFQDGLSYSTFKTITDLFLRDVDTRGESEVKARGFKAALA IDAIAKLTAIDHBPMNALGFTKVLREYFSPWVQQNGGWEKILGISHEEVD" 384 c 399 g 317 t
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/strain="C57BL/6J"
/db_xref="MGD:MGI:1894677"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB30545.1"
/db_xref="GI:12856034"
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/clone_lib="RIKEN full-length enriched mouse
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/clone="4933430L01"
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3 (sites
                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new companion.
                                                                                                                                                                                                                    Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                           Genome Res.
                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                    clone:2210008009.
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AUTHORS

Konno, H.,

TITLE JOURNAL REFERENCE

AUTHORS

REFERENCE

MEDLINE JOURNAL

PUBMED

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AUTHORS

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E 5 (bases 1 to 1541)

S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Alzawa, K., Akahira, S., Erwinstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Tayami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GARAGARGATCCAAKAGCTCTTTTTTTTTTTTTTTTTYN 3, CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with XhoI and SstI. Cloning sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection Nature 409, 685\text{-}690 (2001)
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                                                     putative"
                                                                                                                                                           /tissue_type="stomach"
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/dev_stage="adult"
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/strain="C57BL/6J"
                                                                                    hypothetical
                                                                                                              /note="evidence:NAS
                                                                                                                                                                                                                                                /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                  /db_xref="MGD:MGI:1898348"
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Kitsunai,T., Tashiro,H., Itoh,M.,
                                                                                                                                                                                             enriched mouse cDNA library"
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                            .1 GI:12858357
                                                                                                        clone:9030625M01:hypothetical protein, full insert
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VAEIVYSWPPPDVIHSQGGSKLKERVSEILYFRFEGPCDSKNKDGEDQIISKIVELLK
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IDAIAKLTAIDNHPMNRMLGFGTKYLREYFSPWVQQNGGWEKILGISHEEVD"
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Hayashizaki,Y.

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                                                                                                                                                                                                                                                                                                         Direct Submission

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIEN), Laboratory for Genome Exploration Research Group, RIEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, rurr.htm.//genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                           Functional annotation of a Nature 409, 685-690 (2001) 5 (bases 1 to 1578)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to
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                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                      Fax:81-45-503-9216]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki,Y.
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/db_xref="GI:12858358"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                    FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

E 5 (bases 1 to 2222)

S Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., S Adachi,J., Aizawa,K., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotoni,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                Sogabe, Y., Suzuki, H.,
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Mus musculus (strain:C57BL/6J) adult
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
   Tagami,M., Tagawa,A.,
Toya,T., Yamamura,T.,
                                Tagawa,A.,
      Yamanaka, I.
                                Takahashi, F.,
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121 gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaat 180
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VAEITYSWPPPDVIHSQGGSKLKEWYGEILYFRFEGFCDSKNNKDGEDQIISKTVELKE
KSGDQLGREIKKDKALMSSFQDGLSYSTFKTITDLFLRDVDTRGESEVKARGFKAALA
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                 Score 294.6; DB 11; Length 2222; Pred. No. 2.2e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 GCTGTCTTCTCGCCCAAGCTCTCCAGAACAAGGAGTCTGTCCCAGAAAGCCCTGGGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aacgtggagcagtgcttggagcatgaagctgtggaccccaaagtcatttccattgccaac 465
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                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11679 row: i column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BI463753
                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                      High quality sequence stop: 685
                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:5269331"
                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Catarrhini; Hominidae;
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             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 920)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603174765F1 NCI_CGAP_Mam5 Mus musculus
                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI453888.1 GI:15244544
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http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-Torgan: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (9tcg: ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3' size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for the state of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for full-length clones and constructed using the
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                                                                                                                                                                                                                                                                                           GTGTGGAGCAGCGCCTGGAGAGTGAAGTCGTGGATTCCAAAGTGGCTTGTATTGCCAACA 634
                                                                                                                                                                                                                                                                                                             acgtggagcagtgcttggagcatgaagctgtggaccccaaagtcatttccattgccaacc 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagaaggaagatt---cgcagagcacgcctgccaaggtctctgctcagggtcaaaggacg
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                                                                                                                                                                                                                                                                                                                                                                                             ttggaataccaagattcgcacag-----ccagcagtggtccaggtgtctttcta 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371;
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                                                                AA536718 652 bp

1988a02.rl Knowles Solter mouse 2

IMAGE:944138 3', mRNA sequence.

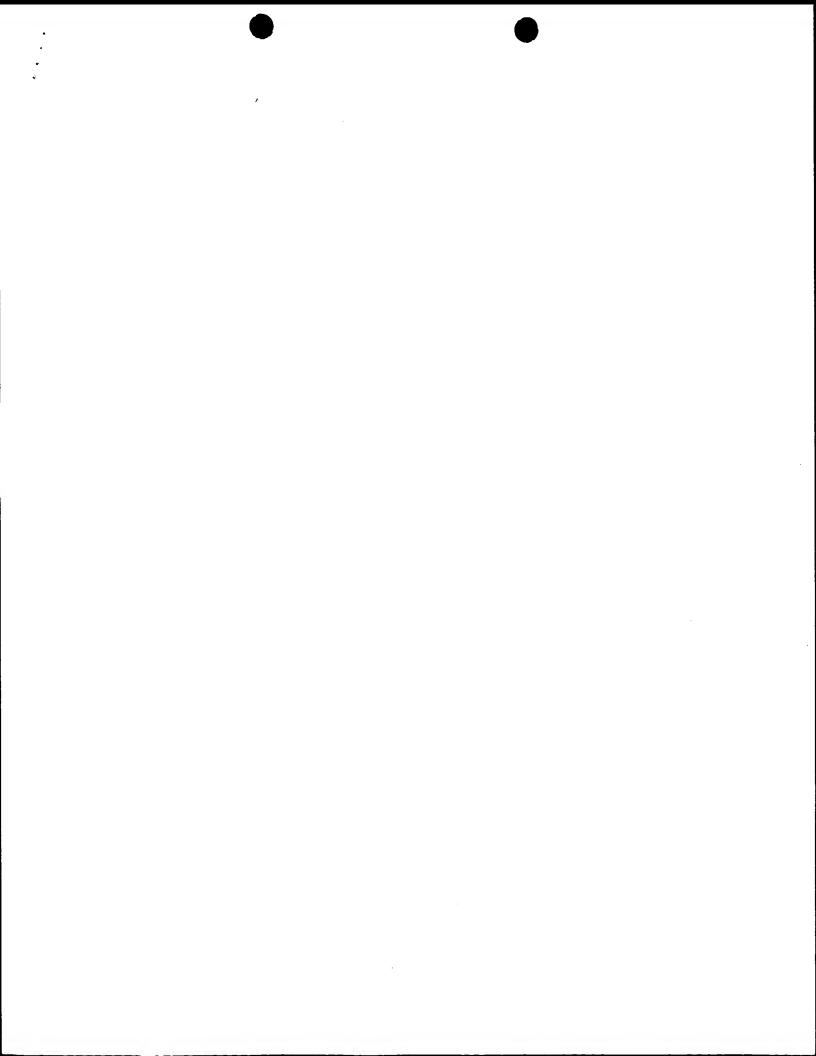
AA536718

AA536718.1 GI:2282711
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Eukaryota;
                                   house mouse.
                musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:5253808"
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/strain="C57/B6"
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 Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 c
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   Vertebrata;
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   Euteleostomi;
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                                                                                                                                         EST 29-JUL-1997
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JOURNAL
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Best Local :
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                                                                                                         301 gaga---aggaagattcgcagagcacgcctgccaaggtctctgctcagggtc-----
                                                                                                                                                                                                                                                                     181 tyttcaycaaatyaytcatyyacayagytytcatyyccttycayaaattcccaatccayt 240
                                                                                                                                                                                                                                                                                                                                                                                                                   147 AGCATAGAGTTCAAAATCCTGGCCTTCTACGCCAGACACCATGTCTTCAAGAACACCCCG 206
                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                        gagaaggccataaaccttggcaagaaaaagtcttcttggaaagcattctttggagtagtg 300
                                                                                                                                                                                                                                                                                                                                                       gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagagggggcctggggaat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                      accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct 120
CCCTTCCCGGTAGAGCGGCAGAGTGGCTTCCACAACCAGCACTGGCCCCAGGTCTCTGAGC 503
                                                                                 GAGAAGGAGGAAGGCCTGCCGNGCTCCCCAAAGGAGATCCGAGCTCAGGGTCCTCAGGGC 443
                                                                                                                                                                     GAAAAGAACATCAGCTTGGGCAAGAAGAAGTCTTCTTGGAGAACACTCTTCAGGGTGGCC 383
                                                                                                                                                                                                                                                  TGGT---CAACTGATTCCTGGACACAGGTATCATTGCCTTGCAGAGGTTCCCCCCTCCAGC
                                                                                                                                                                                                                                                                                                                                  GCTGTCTTCTCGCCCAAGCTCTCCAGAACAAGGAGTCTGTCCCAGAAAGCCCCTGGGGACT
                              ----aaaggacgttggaataccaagattcgcacagccagccagtggtccaggtgtctttct 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381;
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuqu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project WashIngton University School of MedicineP WashIngton to Parkway, Box 8501, St. Lc Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 481
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Knowles Solter
/tissue_type="embryo"
/dev_stage="2-cell"
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/clone="IMAGE:944138"
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72.3%;
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Pred. No. 1.4e-60;
O; Mismatches 127; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse
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Search completed: June 20, 2002, 04:19:27 Job time: 6417 sec



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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             759
757.4
678
676.4
485.6
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                                                                                                                       gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaat
                                                                                                                                                                                                                   accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct
                                                                                            gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaat
                                                                                                                                                                                             accatagaattcaaaaatcctcgcctactacaaccagacatcatgtcttcaagagcacccct
tgttcagcaaatgagtcatggacagaggtgtcatggccttgcagaaattcccaatccagt
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Pred. No. 4.6e-228;
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                  2001-398125/42.
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                                                                                                                                                                                                                                     cancer;
                                                        BURNHAM INST
          AAB85167
                                                                                                                                                                                                                                                                                                                   standard;
                                      Godzik A;
                                                                                                2000WO-US33793
                                                                                                                                                                                                                                                      polypeptide encoding cDNA
                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                            cancer therapy; oncogene;
chromosome 12p12.3; human
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196..954
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/product= "Bcl-Gs"
                                                                                                                                                                                                                                                                                                                  CDNA;
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Novel polynucleotide encoding Bc1-G polypeptide, apoptosis, and for diagnosing and treating cancer polypeptide, useful for modulating

specific antibodies are useful for diagnosing cancer, monitoring cancer therapy or assessing prognosis of patients with cancer. The Bcl-G polypeptides are useful for modulating the activity of an oncogenic polypeptide. They are useful for identifying modulators, for modulating a level of apoptosis mediated by the Bcl-G polypeptide. A therapeutic composition comprising the Bcl-G polypeptide, polynucleotide or antibody is useful for treating a pathology characterized by abnormal cell proliferation especially cancer. The present sequence represents a cDNA ancoding a Bcl-Cs polypeptide. The invention relates to Bcl-G The Bcl-G a Bcl-Gs n relates to Bcl-G polypeptides and nucleic acids encoding l-G polypeptides can be expressed by standard recombinant Bcl-G oligonucleotides (or its anti-sense strand) and Bcl-G polypeptide. acids encoding antibody

Sequence 954 BP; 267 Α; 237 C; 240 G; 210 Τ; 0 other;

ρy δÃ δÃ γ Ъ δÃ γQ Qy Qy Qy DЬ QΥ Вb В Ъ В Ъ 밁 δÃ Вр 밁 뭕 Дb QY Query Match Best Local Matches Local 758; 301 ب ttggagcatgaagctgtgggaccccaaagtcatttccattgccaaccgagtagctgaaatt gaataccaagattcgcacagccagcggtggtccaggtgtctttctaacgtggagcagtgc gatcagttggaaagaaaggacactgccttcatccccattcccttggttgacaccagcatc aagaaagatgaagaacaaatactagccaaaattgttgagctgctgaaatattcagga gtttattcctggccaccaccacgcgacccaggcaggcgttcaagtccaaggaggtt gagaaggaagattcgcagagcacgcctgccaaggtctctgctcagggtcaaaggacgttg gagaaggccataaaccttggcaagaaaaagtcttcttggaaagcattcttttggagtagtg gctcttttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaat atgtgtagcaccagtgggtgtgacctggaagaaatccccctagatgatgatgacctaaac gtttactcctggccaccaccaccagcgacccaggcaggaggcttcaagtccaaagagatt gaataccaagattcgcacagccagcagtggtccaggtgtctttctaacgtggagcagtgc gagaaggaagattcgcagagcacgcctgccaaggtctctgctcagggtcaaaggacgttg gagaaggccataaaccttggcaagaaaagtcttcttggaaagcattctttggagtagtg tgttcagcaaatgagtcatggacagaggtgtcatggccttgcagaaattcccaatccagt accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct 120 aagaaagatgaagaagaacaaatactagccaaaattgttgagctgctgaaatattcagga ttggagcatgaagctgtggaccccaaagtcatttccattgccaaccgagtagctgaaatt tgttcagcaaatgagtcatggacagaggtgtcatggccttgcagaaattcccaatccagt gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaat atgtgtagcaccagtgggtgtgacctggaagaaatccccctagatgatgatgacctaaac Similarity Conservative 99.8%; 0; Score 757.4; DB 22 Pred. No. 9.8e-228; Mismatches Indels Length 954; 0; Gaps 600 480 615 555 495 435 180 60 795 420 360 300 375 0

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RESULT
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                                                                                                                                                                                              Query Match
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Matches 678;
                                                                                                                                                                                                                                                                                                                                                  The present sequence is a cDNA encoding human BCL-X-like protein. The BCL-X-like polynucleotides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of protein in the body and also for treating physiological disorders and diseases. The BCL-X-like polynucleotides are useful in conjunction with polymerase chain reaction to screen libraries, isolate clones, to prepare cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated human BCL-X-like polynucleotide, useful in diagnostic and pharmacogenic applications -
                                                                                                                                                                                                                                                                                   Sequence 984
                                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                              Conservative
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Pred. No. 9.4e-203;
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RESULT
AAS90453
ID AAS9
     Matches
                 Query Match
Best Local Similarity
                                                                                                                             (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                     polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
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food supplement; medical imaging; diagnostic; genetic of
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                                                                                    1917
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Score 485.6; DB 23;
Pred. No. 4.5e-142;
0; Mismatches 9;
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                                                                                              cancer;
                                                                                                        Human;
                                                                                                                               Human reproductive system related antigen cDNA SEQ ID NO: 1349.
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17-JAN-2001; 2001WO-US01339.
                        02-AUG-2001
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                                                                                           reproductive system related
; gene therapy; ss.
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2000US-0230438.
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2000US-0227182.
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01-NOV - 2000;
08-NOV - 2000;
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 Isolated nucleic acid
                                            Rosen
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01-DEC-2000;
                                                            (HUMA-) HUMAN GENOME SCI INC
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                   2001-465570/50.
)В; AAM95378.
                                            CA,
                                            Barash SC,
                                                                             2000US-0251990.
2000US-0254097.
2001US-0259678.
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2000US-0251868.
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2000US-0251988.
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molecule encoding a reproductive system antigen
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Best Local Similarity
                                disease;
                                                                                          01-FEB-2002
                                                                                                                 ABA47100;
                                                                                                                                     ABA47100 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
        Homo sapiens
                                          Human; microarray; single exon probe; gene expression; breast;
                                                                Human breast cell single exon nucleic acid probe #5795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                 cancer;
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-124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                           ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New spatially-addressable set of single exon nucleic acid posseful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid probes for measuring gene expression in a sample derifrom human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 388 BP; 113 A; 91 C; 99 G; 85 T; 0 other;
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                                                                                                                                                                                               aggggcctggggaattgttcagcaaatgagtcatggacagaggtgtcatggccttgcaga
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                                                     ttctttggagtagtggagaaggaaggattcgcagagcacgcctgccaaggtctctgctcag
                                                                                                         aattcccaatccagtgagaaggccataaaccttggcaagaaaaagtcttcttggaaagca
                                                                                                                         aattcccaatccagtgagaaggccataaaccttggcaagaaaaagtcttcttggaaagca
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ttctttggagtagtggagaaggaagattcgcagagcacgcctgccaaggtctctgctcag
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                              51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 388;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon nucleic acid probes, sample derived from human
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Best Local Similarity
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26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
                                                                                                                                                                                                                                                                           measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probe in a predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
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                                                                                                                                                                                                          Sequence 388 BP;
                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direction WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 13287; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
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                                        106 ttcaagagcacccctgctctcttctcaccaaagctgctgagaacaagaagtttgtcccag 165
166 aggggcctggggaattgttcagcaaatgagtcatggacagaggtgtcatggccttgcaga
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                                                                                                                                         388;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                        Conservative
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                                                                                                                                                     51.1%; Score 388; DB 22; 100.0%; Pred. No. 1e-111;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems, cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2090
Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                             congenital heart disease.
                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00666
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                                                                                                                                                                                                                                                                                                                                                                                congenital heart
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                                                                                                                                              exon nucleic acid probes
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                                                                                                                      SEQ ID No 10556; 530pp; English.
                                                                                                                                                                                        Hanzel DK,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236559.
2000US-0236559.
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                                                                                                                                                                                                                                                                                                                                                                                                                   expression analysis in human heart cell sample.
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        format directly from WIPO
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Best Local Similarity
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
27 - SEP - 2000;
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                                                            04-OCT-2000;
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                                                                                                                                                                                                                 09-AUG-2001.
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                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizopt
                                                                                                                                                                                                                                                                                                                                                                    Human brain
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                              MOLECULAR DYNAMICS
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Hanzel DK,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                  expressed single exon
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ilarity 100.0%;
Conservative
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single
brains
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                                            30-JAN-2001;
                                                                                          WO200157276-A2
                                                                                                                                                                      Human bone marrow expressed single exon
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                                                                                                                                      cancer;
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Pred. No. 1e-111;
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                                                                                                                                      lymphoma;
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Matches 388
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing gene expression in
                        cervical cancer;
                                                          Probe #9887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388;
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                                     human;
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                                                                                                                             standard;
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; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
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                                                        for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 113 A; 91 C;
                                                                                (first
                                   microarray;
                                                                                                                             DNA;
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                                                         expression analysis in human cervical cell sample.
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ved from genomic sequences expressed
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                                   gene
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Pred. No. 1e-111;
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                                   expression;
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Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic format directly from WIPS of the cervix as obtained in electronic f
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04-OCT-2000;
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21-SEP-2000;
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30-JUN-2000;
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aacgtggagcagtgcttggagcatgaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
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27-SEP-2000;
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30-JUN-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, staging, monitoring and prognosing diseases of the human breast, include; breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID No 5657; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel single exon nucleic acid probe used in a human breast - \ensuremath{\mathsf{T}}
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Search completed: June 20, 2002, 05:05:37 Job time: 5981 sec

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Listing first 45 summaries
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## ALIGNMENTS

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                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 759)

Donoho,G., Hilbun,E., Turner,C.A., Friedrich,G.B., Abuin,A.,

Zambrowicz,B. and Sands,A.T.

Human bcl-x-like proteins and polynucleotides encoding the same Patent: WO 0157213-A 3 09-AUG-2001;

Lexicon Genetics Incorporated (US)

Location/Qualifiers
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                                           Homo sapiens
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Lexicon Genetics Incorporated (US)
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ttggagcatgaagctgtggaccccaaagtcatttccattgccaaccgagtagctgaaatt
                                                                   gtttattcctggccaccaccacagcgacccaggcaggaaggcttcaagtccaaagagatt 540
                                                                                                                                                          GAATACCAAGATTCGCACAGCCAGCAGTGGTCCAGGTGTCTTTCTAACGTGGAGCAGTGC
                                                                                                                                                                         gaataccaagattcgcacagccagcagtggtccaggtgtctttctaacgtggagcagtgc
                                                    TTGGAGCATGAAGCTGTGGACCCCAAAGTCATTTCCATTGCCAACCGAGTAGCTGAAATT
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Mammalia; Eutheria; Primates;
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VYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKY
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/db_xref="taxon:9606"
196. .954
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J. Biol. Chem. 2
21264734
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1 (bases 1 to 2039)
Guo, B., Godzik, A. and Reed, J.C.
Bcl-g, a novel pro-apoptotic member of the bcl-2 family
J. Biol. Chem. 276 (4), 2780-2785 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-JUN-2000) The Burnham Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guo, B., Godzik, A.
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                                                                                                                                                                                                                                                                                                               /product="apoptosis regulator BCL-G short form"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="member of Bcl-2 family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BCLG"
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Montpetit, A., Boily, G. and Sinnett, D. A. detailed transcriptional map of the chromosome 12p12 tumor
                                                                                     Submitted (14-JUN-2001) Hemato-Oncology, Cote-Ste-Catherine, Montreal, Qc H3T 1C5_Location/Qualifiers
                                                                                                                                                                                                                                                                               Homo sapiens apoptosis complete cds.
AY040274
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Montpetit, A. and Sinnett, D.
                                                                                                                                                       Unpublished
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680; Conservative
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/note="member of the
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DEFINITION

AX207692 Sequence

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GATCAGTTGGAAAGAAAG
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Human bcl-x-like proteins and polynucleotides encoding the same Patent: WO 0157213-A 1 09-AUG-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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1 (bases 1 to 984)
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/db_xref="taxon:9606"
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Reed, J. C. and Godzik, A.
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EDSQSTPAKVSAGGORTLEYQDSHSQQWSRCLSHVEQCLEHEAVDPKYISIANRYAEI
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DVTAKLTAIDNHPMMRVLGFGTKYLKENFSPWIQQHGGWEKILGISHEEVD"
285 c 305 g 249 t
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196. .1179
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99.9%;
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Patent WO0144282.
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                     gatcagttggaaagaaag
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                                                                                                                                                                                                         677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-JUN-2000) The Burnham Pines Road, La Jolla, CA 92037, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guo,B., Godzik,A. and Reed,J.C.
Bcl-g, a novel pro-apoptotic member of the bcl-2 family
J. Biol. Chem. 276 (4), 2780-2785 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF281254 1886 bp mRNA linear PRI 28-JF Homo sapiens apoptosis regulator BCL-G long form (BCLG) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guo, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21264734
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1 (bases 1 to 1886)
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),B., Godzik,A. and Reed,J.C
                                                                                                                                                                                                                                                                                                                                               535
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                          /product="apoptosis regulator BCL-G long form"
/product="apoptosis regul
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196. .1179
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/db_xref="taxon:9606"
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                     Worley,K.C. Direct Submission Direct Submitted (13-MAY-1999) Molecular and Human Genetics, Baylor Submitted (13-MAY-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 190858)
Worley,K.C.
                                                                                                                                                                                                                       Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,
Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,
Gorrell,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S.,
Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W.,
Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A.,
Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,
Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,
Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W.,
Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
                                                                                                                                                                 Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC007537
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Homo sapiens 12p12 BAC RPCI11-267J23
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			AUTHORS TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE
Contig length: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Praction of phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:  Consensus changing edits:  12 Number of N's in consensus changing edits:  13 Number of N's in consensus changing edits:  14 Number of N's in consensus changing edits:  15 Number of N's in consensus changing edits:  16 Number of N's in consensus changing edits:  12 Number of N's in consensus changing edits:  13 Number of N's in consensus changing edits:  14 Number of N's in consensus changing edits:  15 Number of N's in consensus changing edits:  16 Number of N's in consensus changing edits:  17 Number of N's in consensus changing edits:  18824  10 000339024  11 Number of N's in consensus changing edits:  12 Number of N's in consensus changing edits:  12 Number of N's in consensus changing edits:  12 Number of N's in consensus changing edits:  13 Number of N's in consensus changing edits:  14 Number of N's in consensus changing edits:  15 Number of N's in consensus changing edits:  16 Number of N's in consensus changing edits:  17 Number of N's in consensus changing edits:  18 Number of N's in consensus changing edits:  10 Number of N's in consensus changing edits:  12 Number of Consensus changing edits:  12 Number of Consensus changing edits:  12 Number of N's in consensus changing edits:  12 Number of N's in consensus changing edits:  12 Number of N's in consensus changing edits:  14 Number of N's in consensus changing edits:  15 Number of Consensus changing edits:  16 Number of N's in consensus changing edits:	continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.  SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.  OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.	sent onest remainder cloi of to of of to of of to of of to of to of to of of to of to of to of to of to of of to of of to of to of to of to of of to of of to of to of to of of of to of of of of to of of to of of of of of to of of o	MOTIEY,K.C.  Direct Submission  Direct Submission  Submitted (09-CCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  Baylor Plaza, Houston, TX 77030, USA  On May 28, 1999 this sequence version replaced gi:4895156.  INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu	Direct Submission Submitted (27-MAY-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  4 (bases 1 to 190858) Worley, K.C. Direct Submission Submitted (28-MAY-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 190858)

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1 (bases 1 to 194143)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jun 25, 2001 this sequence version replaced gi:13957543.
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Center clone name: RP11-2513

Center clone name: RP11-2513

Sequencing vector: Plasmid; M77789

Sequencing vector: M13; L08821

Chemistry: Dye-primer Bodipy: 7% of reads
Chemistry: Dye-terminator Big Dye: 93% of reads
Chemistry: Program: Phrap; version 0.990329

Consensus quality: 185441 bases at least Q40

Consensus quality: 200072 bases at least Q30

Consensus quality: 208935 bases at least Q20

Estimated insert size: 199196; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sqarose-fp estimation
Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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48692

181

48632

61

Query Match Best Local Similarity

57.4%; 97.4%;

Score 435.8; DB 9; Pred. No. 1.1e-121; Mismatches

DB 9;

Indels

443; Conservative

0;

repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

complement(15646. .15821)
/rpt\_family="MLT1H"

/rpt\_family="L1MD1"

family="Aluy" \_family="L1MD1" repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

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\_family="Alus"
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\_family="L1MEc"

family-"AluSx"

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TTGGAGCATGAAGGTAGGCATCTGGGATTTCTTTC 48966  361

SOURCE

ORGANISM

Homo sapiens

EYWORDS VERSION ACCESSION

AC022222 AC022222.34 GI:14547295 HTG; HTGS\_PHASE1; HTGS\_D

HTGS\_DRAFT

DEFINITION AC022222/c

AC022222 194143 bp DNA linear F Homo sapiens chromosome 12 clone RP11-52513, WORKING SEQUENCE, 26 unordered pieces.

Snoo

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BASE COUNT
ORIGIN
                                                                                                                    FEATURES
         Query Match
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  al Similarity
443; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 26 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved
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                                                                   /clone="RP11-525I3"
                                                                             /chromosome="12"
                                                                                      /db_xref="taxon:9606"
                                                                                               /organism="Homo sapiens"
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187495: contig
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189691: contig
189791: gap of u
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                                                              Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H. H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Erantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Holloway, C., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L. Li, J., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mahashar, V., Mahashar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 200499)
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                                       Metzker, M., Miner, G., Miner, Z., Mitchell, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA On Sep 16, 2001 this sequence version replaced gi:15042773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved.
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Sequencing vector: Plasmid; M77789

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 206551 bases at least Q40

Consensus quality: 20841 bases at least Q30

Consensus quality: 208973 bases at least Q20

Estimated insert size: 203052; sum-of-contegs estimation

Quality coverage: 0x in Q20 bases; sum-of-contigs estimation

Quality coverage: 12.7x in Q20 bases; sum-of-contigs estimation
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Location/Qualifiers
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EGLPXSPKEIRAQGPQGPFPVERQSGFHNQHWPRSLSSVEQPWRVKLWIPKWLVLPTE
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                                                                                                                                     /codon_start=1
                                                                                                                                                     /note="unnamed protein product"
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/db_xref="taxon:10090"
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                                                                                                                                                                                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                      646 ctgaaatattcaggagatcagttggaaagaaag 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgttcagcaaatgagtcatggacagaggtgtcatggccttgcagaaattcccaatccagt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gctctcttctcaccaaagctgctgagaacaagaagtttgtcccagaggggcctggggaat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accatagaattcaaaatcctcgcctactacaccagacatcatgtcttcaagagcacccct 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCAGCTCAAAGAGGGGTCTCGGAGATTTTTGTACTTCAGGTTTGAAGGACCTTGGGA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGTGGCTGAAATTGTTTACTCCTGGCCACCACCAGATGTCATCCACAGCCAGGGAGGA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTGTGGAGCAG-CCCTGGAGAGTGAAGTTGTGGATTCCAAAGTGGCTTGTATTGCCAAC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAAAGAACATCAGCTTGGGCAAGAAGAAGTCTTCTTGGAGAACACTCTTCAGGGTGGCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGT---CAACTGATTCCTGGACACAGGTATCATTGCCTTGCAGAGGTTCCCCCCTCCAGC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGTCTTCTCGCCCAAGCTCTCCAGAACAAGGAGTCTGTCCCAGAAAGCCCCTGGGGACT 180
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                                                                                                                                                 AC097248
AC097248.3 GI:17973829
HTG; HTGS_PHASE1.
                      Muzny, D.M.,
                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                      Rattus norvegicus clone CH230-177C11, *** SEQUENCING
 Alsbrooks,S.L., Amaratunge,H.C.,
                                                                                                                                                                                                                                           AC097248
                                                                                             Eukaryota; Metazoa;
                                                           Rattus
                                                                            Mammalia; Eutheria;
                                        (bases 1 to 149350)
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                      Adams, C.,
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67.7%;
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                                                                          Chordata;
Rodentia;
 Adio-Oduola, B., Ali-osman, F.R., tunge, H.C., Are, J.R., Banks, T.,
                                                                                                                                                                                                                                           149350 bp
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Pred. No. 1.5e-72;
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                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                        Muridae;
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                                                                                           Euteleostomi;
                                                                        Murinae;
, Allen,C.,
Barbaria,J.,
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Dugan Rocha, S., Durbin, K.I., Earnhart, C., Eddgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guovara, W., Gunarathe, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harris, M., Hoylson, M., Hoylson, M., Holloway, C., Homlins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Moyuen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peetry, J., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Ryees, M., Rojas, A., Rojubokan, I., Rolfe, M., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Sunson, R., Wall, R., Wang, S., Ward-Moore, S., Walliamson, A., Wheston, C., Walliams, G., Williamson, R., Washington, C., Walliams, G., Williamson, A., Westson, D., Wooden, S., Wolliamson, R., Washington, C., Walliams, G., Williamson, A., Wheczyk, R., Wooden, S., Wolliamson, A., Walliamson, A., Wallians, S., Walliamson, A., Walliamson, A., Wallians, S., Walliamson, A., Walliamson, A., Wallians, S., Wallians, S., Walliamson, A., Walliamson, A., Walliamson, D., Vinson, R., Woolen, S., Walliamson, A., Walliamson, S., Walliamson, A., Walliamson, A., Walliamson, S., Walliamson, A., Walliamson, S., Walliamson, R., Washington, C., Walliamson, A., Walliamson, S., Walliamson, R., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Unpublished Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R. Direct Submission

JOURNAL TITLE JOURNAL REFERENCE

AUTHORS

Worley, K.C.

(bases 1 to 149350)

TITLE

COMMENT

Submitted (13-OCT-2001) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17064657. Direct Submission Department

Center: Baylor College of Medicine Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Center project name: ----- Project Information

findPhrapLis Center clone name: CH230-177C11 Assembly program: Phrap; version 0.990329First call

Consensus quality: 114307 bases at least Q40 consensus quality: 121845 bases at least Q30 consensus quality: 128763 bases at least Q20 Estimated insert size: 114370; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces

\* arbitrary. Gaps between the contigs are represented as \* runs of N, but the exact sizes of the gaps are unknown \* This record will be updated with the finished sequence is not known and their order in this sequence record is

as soon as it is available and the accession number will

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
AC097248
                   Rattus norvegicus clone CH230-177C11, ***, 64 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Tanigami, A., Fujirara, T., Ono, T., Yamada, K., Fujir, Y., Ozaki, K., Hirao, M., Ohwashi, Y., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
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Homo sapiens ileal mucosa cDNA to mRNA, clone_lib:kaia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2877)
Sugano, S., Suzuki, Y., Ota, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibahara, T., Tanaka, T. and Nakamura, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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/note="cloning vector pME18SFL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIS Alsbrooks, S.L., Anaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Alsbrooks, S.L., Anaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Burkett, C., Burrell, K.L., Byrd, M.C., Garron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17064657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                 Consensus quality: 114307 bases at least Q40 consensus quality: 121845 bases at least Q30 consensus quality: 128763 bases at least Q20 Estimated insert size: 114370; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation quality coverage: Ox in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                       Center project Information
Center project name: GINL
Center clone name: CH230-177C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
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    Genome Center

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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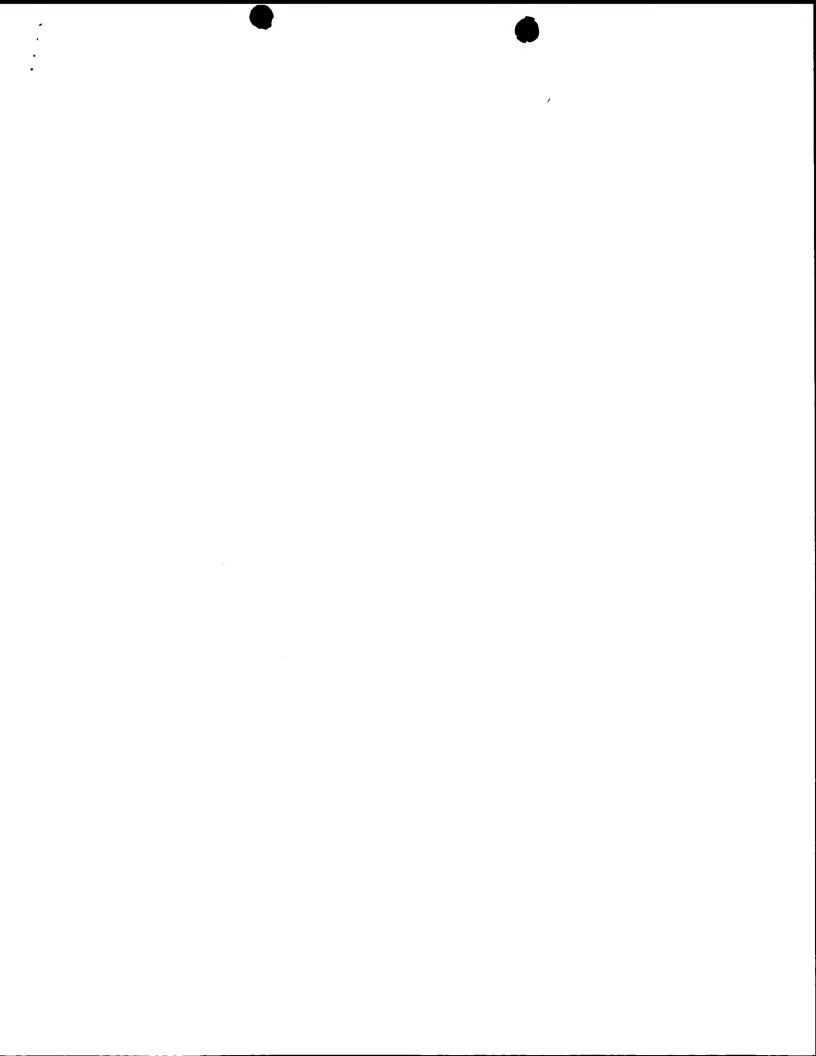
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Search completed: June 20, 2002, 05:11:00 Job time:  $9460 \ \text{sec}$ 



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## ALIGNMENTS

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EMBL; AF281254; AAG59793.1; -.

InterPro; IPR002475; BC12_family.

InterPro; IPR000712; BC1_2.

Pfam; PF00452; BC1-2; 1.

SMART; SM00337; BCL; 1.

PROSITE; PS50065; BCL2_FAMILY; 1.

SEQUENCE 327 AA; 36598 MW; 155D43BA
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O1-DEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
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Q9BZR8;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
apnprosis REGULATOR BCL-G LONG FORM.
    Eukaryota; Metazoa;
                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21264734; PubMed=11054413;
Guo B., Godzik A., Reed J.C.;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                     QGFPQDGL 248
                                                                                                                                                                                                                                                                                                                                                                                                                       QGFPQDGLMACI 252
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Primates;
    Chordata;
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Pred. No. 2.2
    Craniata;
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155D43BA91BFB3EA CRC64;
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    Vertebrata;
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nes 7;
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                                                                               update)
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    Euteleostomi;
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                                                                                                         RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Asaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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Q9CPTO;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
9030625M01RIK PROTEIN (4933405K19RIK PROTEIN).
9030625M01RIK OR 4933405K19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Montpetit A., Boily G., Sinnett D.;
"A detailed transcriptional map of the chromosome 12p12 tumor uppressor locus.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY040274; AAK72109.1; -.
SEQUENCE 276 AA; 30948 MW; 81559A7190F5598E CRC64;
"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK018579; BAB31290.1; -.
EMBL; AK018682; BAB25830.1; -.
EMBL; AK016670; BAB30370.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUE-COLON, STOMACH, AND TESTIS; MEDLINE-21085660; PubMed-11217851;
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                                                                                                     Hayashizaki Y.;
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99.68;
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RX MEDLINE-21085660; PubMed-11217851;

RA MEDLINE-21085660; PubMed-11217851;

RA MEDLINE-21085660; PubMed-11217861;

RA Arakawa I., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa I., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa I., Hara A., Fukunishi Y., Konno H., Kasukawa T., Yamanaka I.,

RA Arakawa I., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Arakawa I., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Arakawa I., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Besole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaert S.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Soto K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaii H., Kohtsuki S., L.,
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                               Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA Nature 409:685-690(2001).
EMBL; AK016997; BAB30545.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
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InterPro;
                                                                                                                                                              Wynshaw-Boris A., Yoshida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDS-QSTPAKVSAQGQR- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:1914063; 9030625M01Rik.
MGI:1914796; 4933405K19Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVDTSIQGFPQDGL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKLKE-RVSEILYFRFEG----PCDSKNKDGEDQIISKIVELLKFSGDQLGREIKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKDTAFIPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFPVERQSGFHNQHWPRSLSSVEQRLESEVVDSKVACIANRVAEIVYSWPPPDVIHSQGG
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; IPR000572; BUK_OXIOOTEd_molyb.
ps50062; BCL2_FAMILY; 1.
ps00559; MOLYBDOPTEXIN_EUK; UNKNOWN_1.
328 AA; 36991 MW; FAC47379F008314C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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4933405K19Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.5%;
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17,
17,
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Last annotation update)
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Pred. No. 7e-53;
                                                                                                                                                                  Hasegawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                              Kawaji H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                  collection.";
                                                                                                                                                                  Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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DR
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            013722;
                                                                                                                                                                                                                                                                                                           Murphy L., Harris D., Wood V., Barrell B.G., F
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: IN THE C-TERMINAL, TO EUKARYOT
INITIATION EACTOR TFIID (TAFII-20).
EMBL; Z97208; CAB10099.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL 07, Created)
01-AUG-1998 (TREMBLREL 07, Last sequence update)
01-JUN-2001 (TREMBLREL 17, Last annotation update)
HYPOTHETICAL 49.2 KDA PROTEIN C15A10.02 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002475; BCL2_family. PROSITE; PS50062; BCL2_FAMILY; 1. SEQUENCE 328 AA; 37036 MW; 79
                                                                                                                                                                                                                             ProDom; PD012998; TFIID_sub; 1. PROSITE; PS00588; FLAGELIA_BB_ROD;
                                                                                                                                                                                                                                               InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR000166; Histone_core.
InterPro; IPR003228; TFIID_sub.
ProDom; PD012998; TFIID_sub; 1.
                                                                                                                                                                                                     Hypothetical
SEQUENCE 45
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPAC15A10.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
 242
                              104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                       Local Similarity les 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                             DSQ--STPAKVSAQ--GQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAE 159
                                                                                       RSLSQRGLGN----CSANESWTEVSWPCRNSQSSEKAI----NLGKKKSSWKAFFGVVEKE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVDTSIQGFPQDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCSTSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DKALMSSFQDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFPVERQSGFHNQHWPRSLSSVEQRLESEVVDSKVAFIANRVAEIVYSWPPPDVIHSQGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | CSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDS-QSTPAKVSAQGQR- 118
TSSVPETPVGVSAANVSNESTELATSATQQ-SGLANNVEKSQTPSYMSANHLPKVDSKSP
                                                           RSIQQ--LQNRQASSANGNNTGTSTPVNASTDTRKSTASTPQLQQTQAQANAPQQRINPE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKLKE-RVSEILYFRFEG---PCDSKNKDGEDQIISKIVELLKFSGDQLGREIKK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TLEYQDS-HSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQA-GG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WS-TDSWTQVSLPCRGSPSSEKNISLGKKKSSWRTLFRVAEKEEGLPSSPKEIRAQGPQG 119
                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                     al protein
450 AA; '
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                     49195 MW;
                                                                                                                                      7.4%;
28.1%;
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57.5%;
                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                    Score 97; DB 3; Length 450; Pred. No. 0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 650; DB 11;
Pred. No. 8.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetes;
                                                                                                                                                                                                     4865CEE7D478B28B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7919C5A4441C62C4 CRC64;
                                                                                                                         Mismatches
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                                                                                                                                                                                                                                  UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450
                                                                                                                                                                                                                                                                                                                                             EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                        Rajandream M.A.;
J databases.
                                                                                                                       94;
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                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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MGD; MGI:1858497; Nope.
InterPro; IPR003961; FN_III_repeat
InterPro; IPR003961; FN_III.
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig.C2.
InterPro; IPR003598; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
INTERPRO; IFR003006; Ig_MHC.
INTERPRO; IFR003047; Ig:4.
INTERPRO; SM00060; FN3; 5.
IMMART; SM000409; IG;4.
SMART; SM00409; IG;4.
SMART; SM00408; IGC2;4.
SMART; SM00409; IG;4.
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Q9EQS8;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBL_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Up-regulation of a ras effector and down-regulation of a cell adhesion molecule are associated with transformation of osteoblasts."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB052621; BAB19279.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-C57BL/CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murakami H., Nakamata T., Nakayama T., Yamamoto H., Hosaka
Aoyama T., Nagayama S., Oka M., Kiyono T., Sasaki M.S., Nal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOPE OR DDM36E.
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                                                                                       649
                                                                                                                             164 W-PPPQATQAGGFK 176
                                                                                                                                                                                589
                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                      483
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                                                                                                                                                                                                                                                                                                                                                                                                                 DLEEIPLDDDDLNT-IEFKILAYYTRHHVFKSTPALFS----PKLLRTRSLSQRGLGNC
                                                                                                                                                                                                                                                                       SPNPSDIRVAWLPLPSSLSNGQVL-----KYKIEYGLGKEEDQVFSTEVPGNETQLTL 588
                                                                                                                                                                                                                                                                                                                     SANESWTEVSW-PCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTL 120
                                                                                                                                                                                                                                                                                                                                                                      DTTELQVRDLEPNTDYEFYVVAYSQLGASRTSSPALVHTLDDVPSAAPQLTLS----- 535
                                                                                    WQPPPHPTQISGYK 662
                                                                                                                                                                                                                         EYQDSHS------QQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYS 163
                                                                                                                                                                              NSLQPNKVYRVRISAGTGAGYGVPSQWMQHRTPGVHNQSHVPFAPAELKVRAKMESLVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEPEVEELLLEIADEFVESVTNF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILAKIVELLKYSGDQLERKDTAF 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPFSVPPSRATLTGGYASGSIGLSTPGLSRAPHYELDNGNRLLSKRKLHDLLQQIDSEEK
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45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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23.2%;
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19,
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 95.5; Di
Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2D55B254A42B9AEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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AC OA8839
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                Q9HCE4
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Best Local
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Pfam; PF00443; UCH-2; 1.
Pfam; PF002148; zf-UBP; 1.
SMART; SM00290; znF_UBP; 1.
PROSITE; PS00973; UCH_2_2; 1.
PROSITE; PS50235; UCH_2_3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA; PubMed-10617197; MEDLINE-20083487; PubMed-10617197; Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carreara A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         048839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thallana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                          1000 YMDTRCSEEDEPVYRLAGLVEHLGAMSRGHYVSYIRGGHKERRDS 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL; AC003974; AAC04485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                         846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLEEIPLDDDDLNTIEFKILAYYTRHHYFKSTPAL----FSPKLLRTRSLSQRGLG 59
                                                                                                                                                                                                    KRDARKKVLINKAPPVLTIHLKRFSQDARGRVSK---
                                                                                                                                                                                                                                               NRVA--EIVYSWPPPQAT-----QAGGFKSKEIFVTEGLSFQLQGHVPV-----
                                                                                                                                                                                                                                                                                             EENTKQAPITSVTETPLLGGETISSQPASDNECENW-----
                                                                                                                                                                                                                                                                                                                                         KEDSQSTP----AKVSAQGQRTLEYQ---DSHSQQWSRCLSNVEQCLEHEAVDPKVISIA 154
                                                                                                                                                                                                                                                                                                                                                                                         NRWVNENGASSAFDECRDSSLNQSCIDL---ENGYKAAPPITKLPNCKEEESAIDDGFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCSANESWTEVSW-PCRNSQSSEKAINLGKKKSSWKAF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSDPAVLDESDSPVSVDRCLAQFTKHEILSEDNAWHCENCSKNLKLQRLREKRRTKEGLS 845
                                                                                                                                                      ---ASSSKKDEEEQILAKIVELL------KYSGDQLERKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083 AA; 120770 MW;
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21.8%;
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Last sequence update)
Last annotation update)
TERMINAL HYDROLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 95;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9;
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                                                                                                                                                                                                                                                                                             -----EDLAVDSEEV-IV 950
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Pfam; PF00047; ig; 1.

PRIMTS PR00014; FNTYPEIII.

SMART; SM00060; FN3; 5.

SMART; SM00409; IG; 1.

SMART; SM00408; IGC; 1.

SMART; SM00410; IG_11ke; 1.

Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO03599; I
InterPro; IPRO03598; I
InterPro; IPRO03600; I
InterPro; IPRO03006; I
                                                                                                                             O18965;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HCE4;
                                                                                                                 EAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 code for large proteins in vitro."; DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KIAA1628 PROTEIN (FRAGMENT).
                                                                                                                                                                                                     018965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O., "Prediction of the coding sequences of unidentified human XVIII. The complete sequences of 100 new cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20450683; PubMed=10997877;
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                                                                                                                                                                                                                                                                                                                               165
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                                                                                                                CHANNEL.
                                                                                                                                                                                                                                                                                             QPPPHPTQISGYK 392
                                                                                                                                                                                                                                                                                                                           -PPPQATQAGGFK 176
                                                                                                                                                                                                                                                                                                                                                               SLQPNKVYRVRISAGTAAGFGAPSQWMHHRTPSMHNQSHVPFAPAELKVQAKMESLVVSW
                                                                                                                                                                                                                                                                                                                                                                                                    SAQGQRTLEYQDSHS-----QQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSW
                                                                                                                                                                                                                                                                                                                                                                                                                                      SPNPSDIRVAWLPLPPSLSNGQVV------KYKIEYGLGKEDQIFSTEVRGNETQLMLN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SANESWTEVSW-PCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAK-----V 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTTELQVRDLEPNTDYEFYVVAYSQLGASRTSTPALVHTLDDVPSAAPQLSLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLEEIPLDDDDLNT-IEFKILAYYTRHHVFKSTPALFS-----PKLLRTRSLSQRGLGNC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB046848; BAB13454.1; -
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47; Conservative
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IPR003961; FN_III.
                                                                                                                             B (TrEMBLrel. B (TrEMBLrel. CTrEMBLrel. CT
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Primates;
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Ig_c2.
Ig_like.
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Last annotation updat
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                                                                                                                             update)
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; Homo.
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brain which
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                           EAG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00100; CNMP; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 1.
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InterPro; IPR001622; Channel_pore_K.
InterPro; IPR001595; cMMP_binding.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
                                                                     "Characterization of ether-a-go-go channels reveals similarity to IKx, a K current in ro J. Gen. physiol. 111:583-599(1998).

EMBL: Y13431; CAA73843.1;
                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000700; PAS-assoc_C. Pfam; PF00027; CNMP_binding; 1. Pfam; PF00520; ion_trans; 1. Pfam; PF00785; PAC; 1.
                                                                                                                                               Baumann A.
                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98190099;
                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                EAG CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                   018966;
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                    InterPro;
                                       InterPro;
                                                      InterPro;
                                                                                                                                                              Frings S., Bruell N.,
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nes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                      Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50042; CNMP_BINDING_3; 960 AA; 108092 MW; 8
   IPR000636; Cation_chan_non_lig
IPR001622; Channel_pore_K.
IPR000595; cNMP_binding.
IPR001610; pAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                             PubMed=9524140;
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                                                                                                                                                              Dzeja
                                                                                                                                                                                                                                                                                                                                                               05,
19,
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                                                                                                                                                           C., Angele A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91.5; Di
Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                            Hagen
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"Characterization of ether-a-go-go channels present reveals similarity to IKx, a K current in rod inner J. Gen. Physiol. 111:583-599(1998).
EMBL; Y13430; CAA73842.1; -.
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SEQUENCE FROM N.A.
MEDLINE=98190099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     733 DLDDLDVEKGSVLTEHSHHGLAKASVVTVRESPATPVAFPAAAAPAGLDHARLQAPGAEG 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQATQAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDDDLNTIEFKILAYYTRHHVFKST-------PALFSPKLL---RTRSLSQRG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKAAGEATLKKTDSCDSGITKSDLRLDNVGEARSPQDRSP-----ILAEVKHSFYPIP 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSAQGQRTLEYQDSHSQQWSRC---LSNVEQCLEHEAVDPKVISIANRVAEIVYS-WP-P 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGPKAGGADCAKRKGWARFKDACGQAEDWSK------VSKAESMETLPER 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQTLQAAVLEVKH------ELKEDIK-ALSTKMTSIEKQLSEILRIL 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LG-----NCSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAK 111
                                                                                                                                                                                                                                                      Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86FCD3303A3E3B08 CRC64;
ls present
rod inner
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segments.";
  segments.
                       in photoreceptors
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                                                                                 Kaupp U.B.,
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10;

InterPro; IPR000014; PAS. InterPro; IPR000700; PAS-

PAS-assoc\_C.

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P
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Q9WZE0
ID Q9WZE0
AC Q9WZE0
DT 01-NOV
DT 01-MAY
DT 11-MAY
DE HYPOTH
GN TM0672
OS Thermo
OC Bacter
OX NCBL_T
RN [1]
RP SEQUEN
RC STRAIN
RY NGELEN
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Best Local S
Matches 49
                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9WZEO;
01-NOV-1999 (TremBLrel. 12, Created)
01-NOV-1999 (TremBLrel. 12, Last sequence update)
01-MAY-2000 (TremBLrel. 13, Last annotation updat
HYPOTHETICAL 74.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                     MEDLINE=99287316; pubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Stewart A.M., Cotton G.G., Fleischmann R.D., Eisen J.A., White O.,
Heidelberg J., Suiton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9WZEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00027; cNMP_binding; 1. Pfam; PF00520; ion_trans; 1. Pfam; PF00785; PAC; 1. SMART; SM00006; PAC; 1. SMART; SM00091; PAS; 1.
                                                                                                                                                                                                                 EMBL; AE001740; AAD35756.1; -.
TIGR; TM0672; -.
Hypothetical protein; Complete proteome.
SEQUENCE 647 AA; 74047 MW; 4CED35D0A761080A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2336;
                                                      128 SSSSKLIKEIKTTDDKSSEKHVLEEVSKRDENHAEYR----KSEQGIFKS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 PQATQAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      864 TKAAGEATLKKTDSCDSGITKSDLRLDNVGEARSPQDRSP-----ILAEVKHSFYPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 VSAQGQRTLEYQDSHSQQWSRC---LSNVEQCLEHEAVDPKVISIANRVAEIVYS-WP-P 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 917 EQTLQAAVLEVKH------ELKEDIK-ALSTKMTSIEKQLSEILRIL 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            820 LGPKAGGADCAKRKGWARFKDACGQAEDWSK-------VSKAESMETLPER 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 DLDDLDVEKGSVLTEHSHHGLAKASVVTVRESPATPVAFPAAAAPAGLDHARLQAPGAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 21.3 es 49; Conservative
                  49 RTRSLSQRGLGNCSANESWTEVSWPCRNSQSSEKA--INLGKKKSSWKAFFGVVEKEDSQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LG-----NCSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 DDDDLNTIEFKILAYYTRHHVFKST------PALFSPKLL---RTRSLSQRG
                                                                                      3 STSGCDLEEIPLDDD-------DLNTIEFKILAYYTRHHVFKSTPALFSPKLL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50042; CMMP_BINDING_3; 1.
987 AA; 110918 MW; 0EF9FB866297DC4F CRC64;
                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.0%;
                                                                                                                                            6.8%;
                                                                                                                         ; Score 89.5; DI
; Pred. No. 8.1;
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
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Pred. No. 9.2;
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647
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                                                                                                                                                               DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                             87;
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                                                                                                                                                             Length 647;
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                                                                                                                             83;
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                                                                                                                             Gaps
                                                        173
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                                                                                                                             12;
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DR RT	RA RA	RA RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	RA	R A	RA	RA	R A	RA	RA RA		RP		000	38	80	O E		DJ DJ		RESULT Q9VK07	Дb	Qy	Db	Qy	Db	Qy	Db
yenc Se 2	eng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith	iams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao ., Yeh R.–F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.,	Wang ZY., Wassarman D.A., Weinstock G.M., Weissenbach J.,	Spradling A.C., Stapleton W., Strong R., Sun E.,	ciden-Kiamos T Simpson M Shunski M D Smith T	lo M., Pittman G.S., Pan S., Pollard J., Puri V., Rees	SON D	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	x Mattel B. McIntosh T.C. McIeod M.D. McDherson D.	.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai	D., Houston K.A., Howland T.J., Wei M. +H., Ibegwam C.,	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann	os B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	erry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P	J., Brokstein P., Brottier P.,	kov s	Hallew R.M. Hasu A. Haxendale J. Havraktarodlu L. Heaslev E.M.	G., Nelson C.R., M	Brandon R.C., Rogers YH.C., Blazej R.G., Champe M., Pfeiffer B.D.,	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,		A., Evans C.A.,	. hbuo.d-1073113	SEQUENCE FROM N.A.	NCBI_TaxID=7227;	a; Drosophilidae; Drosophila.	Eukaryota: Neontera: Endontervoota: Dintera: Brachycera: Muscomornha: Dtervoota: Neontera: Endontervoota: Dintera: Brachycera: Muscomornha:	hila melanogaster (Fruit fly).	CG6116.	(TrEMBLrel. 13, Last annotation	(TremBirel, 13, Created)	1) FAL, 03	13	315TGNEIKMSKLSFVPLLPADEKQQSSNGDG 343	LERKDTA	279 ETRSLPQNSDAAKL-SRDFEKTTGIKNELFEERITGN 314	156 RVAEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVEL 215	230 SESNKKLSSSFRTPAEPSLKSESTKYFKEQPISAQDKETKHSARQPIFN 278	107 STPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIAN 155	174 RTHDISTEKLLTSTEHEEKKENGFLYKDSENKESASQISFEKKHSSIPYLESETSR 229

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Q9EOS9
ID Q9EOS9
AC Q9EOS9
AC Q9EOS9
AC Q9EOS9
DT 01-MAR
DT 01-DEC
DT 01-DEC
DE DDM36.
GN NOPE C
OS Mus mu
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RN [1
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                                                         Query Match
Best Local S
Matches 46
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Best Local Similarity
                                                                                                                                                            Pfam; PF00041; fn3; 5.

Pfam; PF00047; ig; 4.

PFANTS; PR00014; FNTYPEIII.

SMART; SM00060; FN3; 5.

SMART; SM00409; IG; 4.

SMART; SM00408; IGC2; 4.

SMART; SM00410; IG_like; 2.

Immunoglobulin domain; Repeat.

SEQUENCE 1252 AA; 134764 MW; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Up-regulation of a ras effector and down-regulation of a cell adhesion molecule are associated with transformation of osteoblasts."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murakami H., Nakamata T., Nakayama T., Yamamoto H.,
Aoyama T., Nagayama S., Oka M., Kiyono T., Sasaki M.
Toguchida J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOPE OR DDM36.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9EQS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB052620; BAB19278.1; -. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9EQS9;
                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1858497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                       (nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 TQAG------GFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 -EVEQRHKDVFGR------SQLTP---SRLPRPPELLFSWGVYFSGLIPLSPLTL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 LEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSW------PPPQA 169
                                                              Local Similarity
les 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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                       в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCDLEEIP-----LDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLG
                     DLEEIPLDDDDLNT-IEFKILAYYTRHHVFKSTPALFS-----PKLLRTRSLSQRGLGNC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQCGRNCLVFQLNGEQFASPSMISEQALQSQLHLHYQKYAEEEKLEEPQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICTDDEAWRKTNAQC-----VCVKV-----WKHY--SAERRDGQPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFNIESWPHEKSLELDDPD------DVLLYYTL-HTDKASEAFYTSEKLPQRHQQQKWAE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
  <del>..</del>
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696 AA; 80690 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          IPR003962; FnIII_repeat.
IPR003961; FN_III.
IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                     IPR003600;
IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                               IPR003598;
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                                                              Conservative
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                                                                             6.8%;
23.7%;
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Ig_like.
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                                                                                                                                                                                                                                                                                                                                                _IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                              26;
                                                            Score 89; DB
Pred. No. 22;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.5; E
Pred. No. 8.9;
Pred. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2E6FDA367CF8D0CD CRC64;
                                                                                                                                                                   BA5292393483AB73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1252
                                                                                                    DB 11; Length 1252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
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I.S., Nak
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                                                              40;
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Q9JLI1
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Db
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648
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Best Local
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00041; fn3; 5.

Pfam; PF00047; ig; 4.

Pfam; PF00047; ig; 4.

PRINTS; PR00014: FNTYPEIII.

SMART; SM00060; FN3; 5.

SMART; SM00408; IGc2; 3.

SMART; SM00410; IG_like; 1.

Immunoglobulin domain; Repeat.

SEQUENCE 1252 AA; 134759 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9JLI1
Q9JLI1;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin superfamily related Genomics 64:15-23(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEIGHBOR OF PUNC Ell PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF176694; AAF65930.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salbaum J.M., Kappen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20175427; PubMed=10708514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-FVB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                            588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 DTTELQVRDLEPNTDYEFYVVAYSQLGASRTSSPALVHTLDDVPSAAPQLTLS-----
164 W-PPPQATQAGGFK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 WOPPPHPTQISGYK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 W-PPPQATQAGGFK 176
                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ); MGI:1858497; Nope.

!cerpro; IPR003962; FNIII_rep.

!cerpro; IPR003961; FN_III.

!cerpro; IPR003598; Ig_c2.

!cerpro; IPR003600; Ig_like.

!cerpro; IPR003006; Ig_MHC.
                                                                                                                                                           SANESWTEVSW-PCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTL 120
                                                                                                                                                                                                                 DTTELQVRDLEPNTDYEFYVVAYSQLGASRTSSPALVHTLDDVPSAAPQLTLS----- 535
                                            NSLQPNKVYRVRISAGTGAGYGVPSQWMQHRTPGVHNQSHVPFAPAELKVRAKMESLVVS 647
                                                                                                                            SPNPSDIRVAWLPLPSSLSNGQVL------KYKIEYG-LGKEDQVFSTEVPGNETQLTL 587
                                                                                                                                                                                                                                                           DLEEIPLDDDDLNT-IEFKILAYYTRHHVFKSTPALFS----PKLLRTRSLSQRGLGNC
                                                                                      EYQDSHS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSLQPNKVYRVRISAGTGAGYGVPSQWMQHRTPGVHNQSHVPFAPAELKVRAKMESLVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANESWTEVSW-PCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P56276; 1TLK.
                                                                                                                                                                                                                                                                                                      1 Similarity
46; Conserv
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                     6.8%;
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                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                 Score 89; DB
Pred. No. 22;
26; Mismatches
                                                                                      -QQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              11948773277B76B2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to guidance receptors.";
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                                                                                                                                                                                                                                                                                                                                           DB 11; Length 1252;
                                                                                                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                      40;
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WQPPPHPTQISGYK 661

Search completed: June 19, 2002, 16:39:46 Job time: 399 sec

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Title:
Perfect score:
Sequence:
                                                                                                                                   Run on:
                                                                                                                                                                      OM protein - protein search, using sw model
US-09-771-961-4
1316
1 MCSTSGCDLEEIPLDDDDLN......IPLVDTSIQGFPQDGLMACI 252
                                                                                   June 19, 2002, 16:40:06; Search time 15.65 Seconds (without alignments) 623.471 Million cell updates/sec
                                                                                                                                                                                                                                 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

rched: 105224 seqs, 38719550 residues

otal number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

7 6 5 4 4 3 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.	
91.5 89.5 889.5 888.5 87 87 885.5 85.5 85.5 86.8 85.5 86.8 87 80.5 80.	Score	
	ery tch	de
431 433 1131 486 520 639 250 250 2639 264 464 464 1464 1468 1469 1653 1777 1777 1789 1184 1189 1189 1189 1189 1189 1189 11		
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AKA6_HUMAN KARI_YEAST UVRG_DROME AC15_MOUSE TECI_YEAST TDT_BOVIN GGA1_HUMAN YC97_HUMAN YC97_HUMAN YC97_HUMAN YC97_HUMAN YC97_HUMAN YC97_HUMAN N153_RAT GLND_ECOLI CLH_YEAST RB12_HUMAN N153_RAT GLND_ECOLI GLH_WEAST RB2_HUMAN N153_RAT GLND_ECOLI YEAST RB2_HUMAN N153_RAT GLND_ECOLI YEAST RB2_HUMAN RL6_MICLU SYGB_BUCAI MSH6_YEAST AKA6_RAT FLDL_VIBPA GGA3_MOUSE YG9L_HUMAN SYA_MYCGE CAS3_MOUSE YG9L_PEAST AKA6_RAT FLDL_VIBPA GGA3_HOUSE YG9L_PEAST AKA6_RAT GGA3_HOUSE CAS3_MOUSE CAS3_MOUSE DC11_DROME DC11_DROME DC13_DROME DC11_HUMAN BAR1_HUMAN BAR1_HUMAN BAR1_HUMAN BAR1_HUMAN BAR1_HUMAN BAR1_HUMAN	ID TDT_MOUSE	
Q13023 homo sapien P11927 saccharomyc Q3yk07 drosophila P35601 mus musculu P18412 saccharomyc P06526 bos taurus Q9ujy5 homo sapien Q9ujy5 homo sapien Q9ujy5 homo sapien Q9ujy5 homo sapien P44654 dictyostell Q16959 anthocidari P13382 saccharomyc P28976 tomato sapien P49791 rattus norv P27249 escherichia P22137 saccharomyc P29375 homo sapien P49734 saccharomyc P29375 homo sapien P33099 micrococcus P57235 buchnera ap Q038375 vibrio para Q038475 vibrio para Q9nz52 homo sapien P47534 mycoplasma Q02862 mus musculu P47046 saccharomyc P18169 drosophila Q03825 saccharomyc P18171 drosophila Q03825 saccharomyc P35251 homo sapien Q9728 homo sapien Q9728 homo sapien	Description P09838 mus musculu	

45	44	43	42	41	40	39	38	37	36	35	34
76	76	76	76	76.5	76.5	77	77	77	77	77.5	77.5
5.8	ت. 8	5. 8	5. 8	5. 8	5. 8	5.9	5.9	5.9	5.9	5.9	5.9
950	597	572	486	518	502	1805	906	630	623	1636	1428
_	Н	μ.	<del></del>	Ц	μ.	Н	Н	μ-	Н	H	Ļ
DC12_DROME	SYK AQUAE	GAG_IPHA	YN8U_YEAST	TDT_MONDO	CPJ2_HUMAN	NEST_RAT	PR01_SCHPO	ACH4_RAT	HPC2_YEAST	BUD3_YEAST	YA84_SCHPO
		P04023 hamster int	P53742 saccharomyc	002789 monodelphis	P51589 homo sapien	P21263 rattus norv	Q12381 schizosacch	P09483 rattus norv	Q01448 saccharomyc	P25558 saccharomyc	009773 schizosacch

# ALIGNMENTS

	T. Su
SEQUENCE FROM N.A.  STRAIN-BALB/C; TISSUE=Thymus;  MEDLINE=93219079; pubMed=8464703;  MEDLINE=93219079; pubMed=8464703;  MEDLINE=93219079; pubMed=8464703;  MEDLINE=93219079; pubMed=8464703;  MEDLINE=93219079; pubMed=8464703;  Poliferential splicing in mouse thymus generates two forms of terminal decxynucleotidyl transferase.";  Nucleic Acids Res. 21:1187-1191(1993).  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.  STRAIN=C57BL/6; TISSUE=Thymus;  Benedict C.L., Gliffillan S., Kearney J.F.;  PubMed=11136823;  Benedict C.L., Gliffillan S., Kearney J.F.;  PubMed=11136823;  Benedict C.L., Gliffillan S., Kearney J.F.;  PRELIMINARY CHARACTERIZATION OF ALTERNATIVE FORMS.  He catalytic activity of the short isoform.";  J. Exp. Med. 193:89-99(2001).  PRELIMINARY CHARACTERIZATION OF ALTERNATIVE FORMS.  MEDLINE-96010194; pubMed=7556063;  MEDLINE-96010194; pubMed=756063;  MEDLINE-96010194; pubMed=756063;  MEDLINE-96010194; pubMed=7560103;  MEDLINE-96010194; pubMed=756063;  MEDLINE-96010194; pubMed=756063;  MEDLINE-96010194; pubMed=756063;  MEDLINE-96010194; pubMed=756063;  MEDLINE-96010194; pubMed=756063;  MEDLINE-960	MOUSE  TDT MOUSE  TOT-MAR-1989 (Rel. 10, Created)  Ol-MAR-2002 (Rel. 41, Last sequence update)  Ol-MAR-2002 (Rel. 41, Last sequence update)  Ol-MAR-2002 (Rel. 41, Last sequence update)  DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme)  TDN MOUSE  TDN MOUSE  TOT  MUS MUSCULUS (MOUSE).  MUSCULUS (MOUSE).  ENtaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  MAMAMMAIIa; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  NCBL_TaxID-10090;  TSEQUENCE FROM N.A.  NCBL_TAXID-10090;  TSOLATION AND MEDLINE=86286588; PubMed=3755527;  MIDLINE=86286588; PubMed=3755527;  KOIWAI O., Yokota T., Kageyama T., Hirose T., Yoshida S., Arai K.;  "Isolation and characterization of bovine and mouse terminal deoxynucleotidyltransferase cDNAs expressible in mammalian cells.";  Nucleic Acids Res. 14:5777-5792(1986).

<del>'</del>

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Query Match
Best Local :
AKA6_HUMAN
Q13023; O150:
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PFOU900; DINTERPOLX.

PRINTS; PRO0869; DNAPOLX.

SMART; SM00292; BRCT; 1.

SMART; SM00483; POLXC; 1.

SMART; SM00483; POLXC; 1.

PROSITE; PS00172; BRCT; 1.

PROSITE; PS00522; DNA_POLYMERASE_X; 1.

Transferase; Nucleotidyltransferase; Terminal addition; Magnesium;

Transferase; Nucleotidyltransferase; Terminal addition; Magnesium;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:98659; Dntt.
InterPro; IPR001357; BRCT.
InterPro; IPR002054; DNA_polx.
InterPro; IPR002054; DNA_polx.
Pfam; PF00533; BRCT; 1.
Pfam; PF00966; DNA_polymerasex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X04123; CAA27735.1; --
EMBL; A68670; CAA46834.1; --
EMBL; AF316014; AAK07884.1; --
EMBL; AF316015; AAK07885.1; --
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SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: 2 isoforms; TDT-L(arge)/TdtL (shown here) and TDT-S(mall)/TdtS; are produced by alternative splicing. The TDT-S form is the major form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-X FAMILY SIMILARITY: CONTAINS 1 BRCT DOMAIN.
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                                                                                                                                                                                                                                                                                                                      TEVSWPCRNSQSSE-KAINLGKKKSSWKAF---FGVVEKEDSQSTPAKVSAQGQRTL-EY 122
                                                                                                                                                                                                                                                                                                                                                          DALDILAENDELRENEGSCLAFMRASSVLKSLPFPI----TSMKDTEGI-PCLGDKVK
                                                                                                                               FRRG----
                                                                                                                                                                                                           OSDKSLRFTQMQKAGFLYYEDLVSCVNR----PEAEAVSMLVKEAVVTFLPDALVTMTGG
                                                                                                                                                                                                                                                                               SIIEGIIEDGESSEAKAVLNDERYKSFKLFTSVFGVGLK----TAEKWFRMGFRTLSKI
                                                                                                                                                                  FKSKEIFVTEGLSFQLQGH----VPVASSSKKDEEEQILAKIVELLKYSG
                                                                                                                                                                                                                                            QDSHSQQWSRC-----LSNVEQCLEHEAVDPKVISIANRVAEIVYSW-PPPQATQAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 23.
54; Conservative
                     015028;
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26
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   (Rel. 40, Created)
                                        STANDARD;
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T -> M (IN REF. 2).

L -> F (IN REF. 2).

R -> G (IN REF. 1).

O -> K (IN REF. 1).

E -> O (IN REF. 1).

D -> H (IN REF. 1).

D -> H (IN REF. 1).

D -> C (IN REF. 1).
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l; Mismatches
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Pred. No. 0.
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E6B109DCF39C8107 CRC64;
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AS (IN
                                        2319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530;
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 DOMAIN
CONFLICT
                                                    Repeat.
REPEAT
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                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
A-kinase anchor protein 6 (Protein kinase A anchoring protein (PRKA6) (A-kinase anchor protein 100 kDa) (AKAP 100) (MAKAP).
AKAP6 OR AKAP100 OR KIAA0311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Hippocampus;
MEDLINE=95238446; F
MCCartney S., Littl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Rapiloff M.S., Shillace R.V., Westphal A.M., Scott J.D
"mAKAP: an A-kinase anchoring protein targeted to the
of differentiated myocytes.";
J. Cell Sci. 112:2725-2736(1999).
                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99343692; PubMed=10413680;
                                      DOMAIN
                                                                                                                SMART;
                                                                                                                                                   InterPro;
                                                                                                                                                                    MIM; 604691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AKAP100).
                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: SARCOPLASMIC RETICULUM AND NUCLEAR MEMBRANE IN HEART MUSCLE. PARTICIPATION OF MULTIPLE TARGETING SIGNALS ALLOW CORRECT INTRACELLULAR TARGETING. THESE MAY BE REPEATED MOTIFS RICH IN BASIC AND HYDROPHOBIC AMINO ACIDS, PALMITOYLATED/MYRISTOYLATED MOTIFS OR ALTERNATIVELY SPLICE TARGETING SEQUENCES.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN CARDIAC AND SKELETAL MUSCLE, FOLLOWED BY BRAIN.

MUSCLE, FOLLOWED BY BRAIN.

DOMAIN: RII-ALPHA BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC HELIX, COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURFACE ON THE R-SUBUNIT DIMER.

SIMILARITY: CONTAINS 2 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 270:9327-9333(1995).
FUNCTION: BINDS TO TYPE II REGULATORY SUBUNITS OF PROTEIN KINASE AND ANCHORS/TARGETS THEM TO THE NUCLEAR MEMBRANE OR SARCOPIASMIC RETICULUM. MAY ACT AS AN ADAPTER FOR ASSEMBLING MULTIPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: INTERACTS WITH RII SUBUNIT OF PKA, PHOSPHATASE 2B
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                                                                                                                                 PF00435;
                                                                                                                                                                                                         U17195; AAA92354.2;
                                                                                                                                                                                        AB002309; BAA20770.1;
                                                                                                              SM00150;
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 762
1036
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PKA-RII SUBUNIT
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                                                                             Spang A., Courtney I., Grein K., Matzner M., Schiebel E.;
"The Cdc3lp-binding protein Karip is a component of the half bridge
of the yeast spindle pole body ";
J. Cell Biol. 128:863-877(1995)
II FUNCTION FRANCELEAR AND
EXTRANUCLEAR MICROTUBULES. KARI HELPS LOCALIZE CDC31 TO THE
SPINDLE POLE BODY (SPB), CDC31 THEN INITIATES SPB DUPLICATION VIP
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Obermaier B., Piravandi E.,
Submitted (MAY-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "KAR1, a gene required for function of both intranuclear and extranuclear microtubules in yeast."; Cell 48:1047-1060(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAR1 OR YNL188W OR N1611.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Cell division control protein KAR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAR1
                                                                                                                                                                              MEDLINE-95181541; PubMed=7876310; Spang A., Courtney I., Grein K.,
                                                                                                                                                                                                                                                                                   cerevisiae
                                                                                                                                                                                                                                                                                                duplication of the microtubule organizing
                                                                                                                                                                                                                                                                                                                                MEDLINE=94350199; pubMed=8070654; Vallen E.A., Ho W., Winey M., Ros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87159524;
Rose M.D., Fink G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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01-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEAST
                                                                                                                                                                                                                  STRAIN-S288C;
                                                                                                                                                                                                                                                                  Genetics
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                                                                                                                                                                                                                                                                                   MEDIINE-94350159; runnou v... Rose M.D.;
Vallen E.A., Ho W., Winey M., Rose M.D.;
"Genetic interactions between CDC31 and KAR1, two genes required for
"Genetic interactions between CDC31 and KAR1, two genes required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
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European Bioinformatics Institute.
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                                                                 INTERACTION WITH A DOWNSTREAM EFFECTOR.
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               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQSSEKAINLGKK------KSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1492 V
A; 256663 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                Rinke M., Domdey H.;
EMBL/GenBank/DDBJ da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 91.5;
Pred. No. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> A (IN REF. 2).
; 3D3037AE40FCCFEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71;
                                                                                                                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
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δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UVRG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
        Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Ceiniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adamstides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bollshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorler G. Carra N. S. Gelbart W.M. Glasser K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UVRAG-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROME
                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VK07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UVRG_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M15683; AAA34716.1; -.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $0005132; KAR1.
division; Microtubules; Mitosis.
LICT 199 199 A -> V (IN REF.
ENCE 433 AA; 50653 MW; D65331B3B2B066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTIIELLKDDTDSKEKR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKIVELLKYSGDQLERK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSYYSLEQKPLPNLSAMNNFNDYTDNKEKEETNNNILKFQAQRDPLQILQSEIEMHTKKL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEDNYKIDEDNIENELQF------TPKIKEASILRSSLLGQRNVLNTRNPKS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQKKRELIESKWHRLLFHDKKMVEKKLESLREYERKRMPPRGTDVSSSEQDNSFKISTPT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KESHIKVKPIINNKSSSQRKSSAALRKQLGKPLPLPYLNSPNSDSTPTLQRKEEVFTDEV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLEEIPLDDDDL-NTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGL---GNCSA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSW-----PPPQATQAGGF-----KSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQIL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QDSHSQQWSRCLSN----VEQCL-----EHEAVDPKVISIAN------RVAEIV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NESWTEVSWPCRNSQSSEKAINLGKKKSSWKAF-FGVVEKEDSQSTPAKVSAQGQRTLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A26455; A26455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z71464; CAA96082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Conser
Gabrielian A.E., Garg N.S., Gelbart W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D65331B3B2B068E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., A Kilmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin X., A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., A McIson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., L., Nelson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H., A Nelson D.R., Weinson M., Skupski M.P., Smith T., A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., A Wang Z., Yao Q.A., Weissenbach J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., The Mang C., Zhou X., Smith H.O., A Packet J., Wang S., Wang S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                         _MOUSE STANDARD; PRT; 1131 AA.

AC15_MOUSE STANDARD; PRT; 1131 AA.

P35601;

01-JUN-1994 (Rel. 29, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Activator 1 140 kDa subunit (Replication factor C large subunit)

(A1-P145) (Differentiation specific element binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send are email to license@isb-sib.ch).
   (ISRE-binding protein). RFC1 OR RECC1 OR IBF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0032499; CG6116.
Hypothetical protein; Coiled coil.
DOMAIN 249 282 COILE
DOMAIN 329 398 COILE
SEQUENCE 696 AA; 80690 MW; 2E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003639; AAF53277.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO MAMMALIAN UVRAG.
                                                                                                                                                                                                                                                      160
                                                                                                                                                                                                                                                                                                                             115
                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                      TQAG------GFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQ
                                                                                                                                                                                                                                                                                                                                                            LEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSW------PPPQA
                                                                                                                                                                                                                                                                                                                                                                                                                               NCSANESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFNIESWPHEKSLELDDPD-----DVLLYYTL-HTDKASEAFYTSEKLPQRHQQQKWAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCDLEEIP-----LDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLG
                                                                                                                                                                                                                                                                                                                                                                                              ICTDDEAWRKTNAQC------VCVKV------WKHY--SAERRDGOPP------
                                                                                                                                                                                                                                                  SQCGRNCLVFQLNGEQFASPSMISEQALQSQLHLHYQKYAEEEKLEEPQ
                                                                                                                                                                                                                                                                                                                         -EVEQRHKDVFGR------SQLTP---SRLPRPPELLFSWGVYFSGLIPLSPLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorrell J.H., Gu Z., Guan P., D., Heiman T.J., Hernandez J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89.5; D
Pred. No. 4.3;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2E6FDA367CF8D0CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
 or send
                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LAF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haque S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lossie A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SWISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luckow B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140-kilodalton humans.";
                                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                                                                                                                                               TEMPLATE
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IPR001357;
                    IPR003959;
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EMBL; U01222; AAA21643.1; -. EMBL; X72711; CAA51260.1; -. EMBL; U36441; AAA79698.1; -. EMBL; U07157; AAC52140.1; -. EMBL; U15037; AAB60452.1; -. MGD; MGI:97891; Recc1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 354-528 FROM N.A.
SEQUENCE OF 354-528 FROM N.A.
MEDLINE=90229765; PubMed=1691767;
MEDLINE=90229765; PubMed=1691767; PubMed=1691767
                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Interferon Res. 10:31-31(1990).

-I- FUNCTION: THE ELONGATION OF PRIMED DNA TEMPLATES BY DNA POLYMERASE DELTA AND EPSILON REQUIRES THE ACTION OF THE ACCESSORY PROTEINS PCNA AND ACTIVATOR 1. THE 140 SUBUNIT BINDS TO THE PRIMER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Differentiation-specific element binding protein (DSEB) binds to defined element in the promoter of the angiotensinogen gene require for the irreversible induction of gene expression during differentiation of 373-L1 adipoblasts to adipocytes.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94089669; PubMed=8265586;
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SIMILARITY: BELONGS TO THE ACTIVATOR 1 140 KDA SUBUNIT FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
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(OCT-1994) to the
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Bunz F., Stillman B., Lichter P., Schuetz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                          license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood W.M., Camper S
he EMBL/GenBank/DDBJ
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update
TY transcription activator TEC1.
TEC1 OR ROCI OR YBR0750.
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ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                             expression in Saccharomyces cerevis analysis.";
Mol. Cell. Biol. 10:3541-3550(1990)
                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=90287143; PubMed=2192259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50172; BRCT; 1.
DNA replication; ATP-binding;
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STRAIN-S288C;
                  SEQUENCE FROM N.A.
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Pfam; PF00004;
                                                                                                                             Laloux I., Dubois E., Dewerchin M., Jacobs E.;
"TEC1, a gene involved in the activation of Tyl
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V -> A (IN REF. 5).
N -> S (IN REF. 4).
MISSING (IN REF. 3 AND 4).
S -> N (IN REF. 1).
T -> A (IN REF. 3).
K -> KQ (IN REF. 4).
MW; A6F4F970A7F9EE94 CRC64;
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Pred. No. 9.7;
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C2HC-TYPE (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                          Tyl-mediated gene molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
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BEDIDAC

01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal a

(Terminal addition enzyme)

transferase).

TDT\_BOVIN

STANDARD;

PRT;

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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00554; TEA_DOMAIN; 1.
Transcription regulation; Trans-acting factor; Activator;
DNA-binding; Nuclear protein.
DNA_BIND 127 192 TEA-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M32797; AAA35141.1; -. EMBL; Z35952; CAA85028.1; -. PIR; A35667; A35667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00065; TEADOMAIN. SMART; SM00426; TEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000818; TEA. Pfam; PF01285; TEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91300541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andre B., Cziepluch C., Vissers S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD; S0000287; TEC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T01084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEA DOMAIN
                                                                                                   192
                                                                                                                                                                                                   156
                                                                   271 LITPITASNEKKIENFI 287
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                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 66:11-12(1991).
EUNCTION: TEC1 IS INVOLVED IN THE ACTIVATION OF TY1 AND FUNCTION: TECH EXPRESSION. IT IS NOT INVOLVED IN MATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 1 'TEA' DNA-BINDING DOMAIN.
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                                                                                                                                                                                                KIRNANFG---RNELISLYIKHKTNEFRTKKQISSHIQVWKKTIQNKIKDSLTLSSKEKE 212
                                                                                                                                                                                                                                                                                                                                                               STSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFK------STPALFSPK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEA domain: a novel, highly conserved DNA-binding motif.";
                                                                                                GHVPVASSSKKDEEEQI
                                                                                                                                                                                                                                                                QRKNEVPNISVSNYFPGQSSETSSTTE-SWTIGCDKWSEKVEEAFLEALRLIMKNGTTKI 155
                                                                                                                                                                                                                                                                                              LLRTR----SLSQRGLGNCSANESWTEVSWPCRNSQSSEK------AINLGKKKSSWK- 94
                                                                                                                                                                                                                                                                                                                                STAACVKNEA---EDNINLID-----THPQFELVNTGLGAKSDDLKSPSAKATFTDK 96
                                                                                                                                 LLHLIEHGAEQTTENSNLFYDIFEEIIDSL--PSVSDSGSLTPKNLYVSNNSSGLSVHSK 270
                                                                                                                                                              VISIANRVA----TEGLSFQLQ 191
                                                                                                                                                                                                                  ----AFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLSN-VEQCLEHEAVDPK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pean Bioinformatics Institute. There are no rest
non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=2070413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55157 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hein C.,
                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                            Score 88; DB 1; Length 486; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F247016D3E75C454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jauniaux J.C., Urrestarazu
                                                                                                                                                                                                                                                                                                                                                                                             95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
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OR TOT.

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                                                                                                                                          A Pandey V., Modak M.J.;

If "Blochemistry of terminal deoxynucleotidyltransferase. Affinity of Indething and identification of the deoxynucleoside triphosphate of binding domain of terminal deoxynucleotidyltransferase.";

I Biol. Chem. 263:3744-3751(1988).

C. TUNCTION: TEMPLATE-INDEPENDENT DNA POLYMERASE WHICH CATALYZES THE CHANDOM ADDITION OF DEOXXNUCLEOSIDE 5'-TRIPHOSPHATE TO THE 3'END OF A DNA INITIATOR. ONE OF THE IN-VIVO FUNCTION OF THIS ENZYME IS THE CHANDOM CONTROL OF MUCLEOTIDES AT THE JUNCTION (N REGION) OF REARRANGED CC IG HEAVY CHAIN AND T CELL RECEPTOR GENE SEGMENTS DURING THE CC HEAVY CHAIN AND T CELLS.

C. CATALYTIC ACTIVITY: N deoxynucleoside triphosphate + (deoxynucleotide)(M) = N diphosphate + (deoxynucleotide)(M+N).

CC -: SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-X FAMILY.

CC -: SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                     Query Match
Best Local
                                                    Matches
                                                                                                                                                                                                                                                               InterPro; IPR001357; BRCT.
InterPro; IPR002054; DNA_Polx.
Pfam; PF00533; BRCT; 1.
Pfam; PF00956; DNA_PolymeraseX; 1.
PRINTS; PR00869; DNAPOLX.
                                                                                                                                                                                                                                                                                                                                                   EMBL; X04122; CAA27734.1;
EMBL; M26146; AAA87354.1;
PIR; A23595; A23595.
PIR; A29948; A29948.
                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                          SEQUENCE
                                                                                                                                                         Transferase; Nucleotidyltransferase; Terminal addition; Magnesium DOMAIN 38 135 BRCT.
                                                                                                                                                                                        SMART; SM00292; BRCT; 1.
SMART; SM00483; POLXC; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS00522; DNA_POLYMERASE_X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressible in mammalian cells.
Biochem. Biophys. Res. Commun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-13 FROM N.A. MEDLINE-87213162; PubMed-3579900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koiwai O., Yokota T., Kageyama T., Hirose T., "Isolation and characterization of bovine and deoxynucleotidyltransferase cDNAs expressible Nucleic Acids Res. 14:5777-5792(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88153669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE OF 221-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of human terminal deoxynucleotidyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86286588; PubMed=3755527;
Koiwai O., Yokota T., Kageyama T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koiwai O., Kaneda T., Morishita R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
              CDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANES
                                                   Similarity
57; Conser
                                                                                                                                          520
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=3346221;
                                                                                                                                          59670 MW;
                                                                     6.6%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Commun. 144:185-190(1987)
                                                                                                                                                                                                                                                                                                                                                                                           .'
                                                 32;
                                                                     Score 87; Pred. No.
..
                                                                                                                                        258FE25B4E77A390 CRC64
                                                   Mismatches
                                                                                     DB 1;
                                                   74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse terminal
in mammalian cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshida S.,
                                                                                     Length 520
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arai K.;
                                                   80;
                                                   Gaps
                  66
                                                   14;
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Strausberg

(NOV-2000) to

the EMBL/GenBank/DDBJ databases.

TISSUE=Neuroblastoma;

SEQUENCE OF 272-369 FROM

N.A.

Wambutt R., Heubner D., Submitted (AUG-1999) to

to

Mewes H.-W., the EMBL/Gen

EMBL/GenBank/DDBJ

Gassenhuber J., Wi Bank/DDBJ databases

Wiemann

. s

TISSUE=Testis;

Matthews

PARTIAL SEQUENCE FROM

N.A.

(ISOFORMS 1

AND

2

[4]

vacuole/lysosome."

Cell Biol.

149:67-80(2000).

Submitted

(DEC-1999) to

the EMBL/GenBank/DDBJ

databases

"A family of proteins with gamma-adaptin and VHS domains the facilitate trafficking between the trans-Golgi network and

Bright N.A.,

Totty N.,

Seaman M.N.J.,

that

Robinson M.S.; Hirst J., Lui W.W.Y.,

SEQUENCE OF 31-639 FROM N.A. (ISOFORM 1).

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FRACE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UJY5; Q9UGW0; Q9UGW1; Q9UGV0; Q9BW94;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP-ribosylation factor binding protein GGA1 (Golgi-localized, gamma ear-containing, ARF-binding protein 1) (Gamma-adaptin related proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20214818; PubMed-10749927; Boman A.L., Zhang C.-J., Zhu X., Kahn R.A.; "A family of ADP-ribosylation factor effectors that can alter transport through the trans-Golgi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=20211637; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dell'Angelica E.C., Puertollano R., Mullins C., Agu Vargas J.D., Hartnell L.M., Bonifacino J.S., "GASs: A family of ADP ribosylation factor-binding adaptors and associated with the Golgi Complex."; J. Cell Biol. 149:81-94(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dell'Angelica E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20211638; PubMed=10747089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGA1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 CIIEEI---IEDGESSEVKAVLNDERYQSFKLFTSVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISOFORM 1).
PubMed=10747088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639
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i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GVG-LKTSEK
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RESULT 9
YC97_HUMAN
ID YC97_HUMAN
AC Q9Y3A5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD003686; HRS; 1.
ProDom; PD021457; G_adapt_C;
SMART; SM00288; VHS; 1.
PROSITE: PS50170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02883; Alpha_adaptinC2; 1. Pfam; PF03127; GAT; 1. Pfam; PF00790; VHS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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DOMAIN 17
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InterPro; IPR002014; HRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                         143 GIVKSDPKLPDDTTF-PLP 160
                                                                                                                                          220
                                                                                                                                                                                                         160 IVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYS 219
                                                                                                                                                                                                                                                                                                                                             73 PCRNSQSSEKAINLG----KKKSSWKAFFGVVEK--EDSQSTPAKVSAQGQRTLEYQDSH 126
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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SUBUNIT: BINDS TO ACTIVATED ARF3.
SUBCELLULAR LOCATION: TRANS-GOLGI NETWORK.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBLQUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 GAMMA ADAPTIN C-TERMINAL DOMAIN.
SIMILARITY: CONTAINS 1 VHS DOMAIN.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF MEMBRANE TRAFFIC
                                                                                                                                      G----DQLERKDTAFIPIP 234
                                                                                                                                                                          LLYSW-----
                                                                                                                                                                                                                                           PQEWEAIQALTVLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVKNKILE
                                                                                                                                                                                                                                                                             SQQWS--RCLSNVEQCLEH------EAVDPKVI-----SIANRVAE 159
                                                                                                                                                                                                                                                                                                             PAMEPETLEARINRATNPLNKELDWASINGFCEQLNEDFEGPPL----ATRLLAHKIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF218584; AAF42847.1; -. AF33521; AAF35393.1; -. AL7_INIT. AL035496; CAB63441.1; ALT_INIT. AL035496; CAB63440.1; ALT_INIT. AL110219; CAB53679.1; -. BC000538; AAH00538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF190862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50179; VHS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR004152; GAT.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF05707.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Goigi stack; (
147 VHS.
274 BINI
230 COII
239 COII
299 GAMM
625 GAMM
545 POLY
101 MISS
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20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70384 MW;
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                                                                                                                                                                      ----TVGL---
                                                                                                                                                                                                                                                                                                                                                                                 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDS TO ARF3.

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

GAMMA-ADAPTIN C-TERMINAL.

POLY-VAL.

MISSING (IN ISOFORM 2).

DN -> HE (IN REF. 6).

MB; B0B6F0B9FAOF7DD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 1; Length 639 Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil; Alternative splicing
                     250 AA
                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                      ---PEEVKIAEAYQMLKKQ 142
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                    CAP_DICDI STANDARD; PRT; 464 AA P54654; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                          CAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein CGI-97.
Homo sapiens (Human)
                actin.
                     Noegel A.A.;
"Identification of a cyclase-associated protein (CAP) homologue in Dictyostelium discoideum and characterization of its interaction with actin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prom; PRO11/2; UPF0023; 1.
ProDom; PD009796; UPF0023; 1.
PROSITE; PS01267; UPF0023; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-20272150; PubMed-10810093;

Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin

Lai C.-H., Chou C. D., Ch'ang L.-Y., Liu C.-S., Lin

"Identification of novel human genes evolutionarily
Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
                                                                                Gottwald U.,
                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                       Adenylyl cyclase-associated protein (CAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 250 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002140; UPF0023.
Pfam; PF01172; UPF0023; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                  MEDLINE=96228685; PubMed=8688557;
                                                                                                                      STRAIN-AX3
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF151855; AAD34092.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE UPF0023 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                   169
                                                                                                                                                                                                                                                                                                                                                                                                                                                185 GLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYSGDQLE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 QSSEKAINLGK----KKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQ--QWS 131
                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                              RAHMRLRFILPVNEGKKLKEKLKPLIKVIESEDY-GQQLE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCLSN--VEQCLEHEAVDP-KVISIANRVAEIVYSWPPPQATQAGGF----KSKEIFVTE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTHSVFVNVSKGQVAKKEDLISAFGT---DDQTEICKQILAKGEVQVSDKERHTQLGQMF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDIATFVADKCVNPETKGPYTVILIERAMKDIHYLVKPNKSTKQQALEVIKQLKEKMKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
Cell 7:261-272(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                    Brokamp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.5%; Score 85.5; D
25.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28788 MW;
                                                                                  R.,
                                                                                  Karakesisoglou I., Schleicher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6EA46C5E3487C3F9 CRC64;
                                                                                                                                                                                                                                                           update)
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Best Local
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                                                                                                                                                                                            Q16959;
Q16959;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
            MEDLINE-96059480; PubMed-7579688;
Ogawa K., Kamiya R., Wilkerson C.G., Witman G.B.;
Ogawa K., Kamiya R., Wilkerson C.G., Witman G.B.;
"Interspecies conservation of outer arm dynein intermediate chain sequences defines two intermediate chain subclasses.";
Mol. Biol. Cell 6:685-696(1995).
-i- FUNCTION: MICROTUBULE-BINDING PROTEIN THAT MAY BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO01837; CAP. Pfam; PF01213; CAP; 1
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                                                                                              TISSUE=Egg
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                    Anthocidari
                                                                                                                                                                Echinoidea;
                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                        Anthocidaris crassispina (Sea urchin)
                                                                                                                                                                                                                                                                          DYI2_ANTCR
                                                                                                                                                                                                                                                                                       ANTCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane; Actin-binding.
DOMAIN 33 42
DOMAIN 217 253
SEQUENCE 464 AA; 4964:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DictyDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U43027; AAB09713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                     NCBI_TaxID=7629;
                                                                                                                                                                                                                                                                                                                                            394
                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                          145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
ified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CELL MEMBRANE.

DOMAIN: THE C-TERMINUS IS RESPONSIBLE FOR SEQUESTERING G-ACTIN
THE N-TERMINUS IS REQUIRED FOR THE PIP2 MODULATION OF CAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE CAP FAMILY.
  DYNEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MAY HAVE A REGULATORY BIFUNCTIONAL ROLE. BINDS G-ACTIN AND PIP2. INVOLVED IN MICROFILAMENT REORGANIZATION NEAR THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE IN A PIP2-REGULATED MANNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                          PSIAIDKTSGCQIYLSKDSLETEIVSSKSSEMNVLIPGATENDDLVELAIPEQYKTSVKG
                                                                                                                                                                                                                                                                                                                                                                       PVASSSK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STPAL-FSPKLLRTRSLSQRG-----LGNCSANESWTEVSWPCRNSQSSEKAINLGKKK
                                                                                                                                                                                                                                                                                                                                                                                               ----SLVQIKGKVNAITLDGCKKTSIVFE-----NAISSCEVVNCNGVEIQVTGRV
                                                                                                                                                                                                                                                                                                                                                                                                                       AVDPKVISIANRV-----AEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVVKAADTKVAKVDAPSRPAVFALQGNKWSIEYQVNNKETVIAEPDSRQTVYIFQCVN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSWKAFFGVVEKEDSQSTPAKVSAQGQR-TLEYQDSH-----SQQWSRCLSNVEQCLEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPAAPVAPAVSSTPVESKKGPGLGAVFGELSKGDGVTSGLKKVTNDMKSK----NFTDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0000012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01088; CAP_1; 1.
PS01089; CAP_2; 1.
 OUTER
                                                                                                                                                                Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                             Echinodermata; Eleutherozoa; Echinozoa; Echinozoa; oidea; Echinacea; Echinoida; Echinometri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.5%;
                                                                                                                                                                                                                                                                                                                                                                    -KD--EEEQILAKIVELLKYSGDQLERKDTAFIPIP-LVDTSIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85.5; DE
Pred. No. 5.6;
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-SER
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                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7ABDD05D8A0148B4 CRC64;
 THE
 AXONEME
                                                                                                                                                                                                                                                                           702 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99;
(BY
                                                                                                                                                                Echinometridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 464;
 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
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DPOA_YEAST
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Best Local
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                                                                                                                                                                                                                                                         DPOA_YEAST
P13382;
01-JAN-1990
01-OCT-1996
16-OCT-2001
STRAIN=S288C / FY1679;
MEDLINE=96267765; PubMed=8701612;
                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                Pizzagalli A., Valsasnini P., Plevani P., Lucchini G.; "DNA polymerase I gene of Saccharomyces cerevisiae: nucleotide sequence, mapping of a temperature-sensitive mutation, and prohomology with other DNA polymerases.";
                                                                                                                     MEDLINE=88234507; PubMed=3287376;
                                                                                                                                                                                                                                            DNA polymerase alpha catalytic subunit (EC
                            SEQUENCE FROM N.A
                                                     Proc. Natl.
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                   POL1 OR CDC17 OR YNL102W OR N2181.
                                                                                                                                                                                                                                                                                                                                                                                    269
                                                                                                                                                                                                                                                                                                                                                                                                            217 KYSGDQLER 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PPPRANFSSTANQWEIYDAYMEDLEKQEKAKEKKAAPSKKDDDKS--KKKLTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                         (Rel. (Rel. (Rel.
                                                     Acad.
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STANDARD;

1468 AA

268

34, Last sequence update)
40, Last annotation updat

update)

2.7.7.7) (DNA polymerase

13, Created)

Sci. U.S.A. 85:3772-3776(1988).

protein

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R PROSITE; PSOUDS, ... PROPERTS_2; 1.

R PROSITE; PS50082; WD_REPEATS_2; 1.

R PROSITE; PS50082; WD_REPEATS_REGION; 1.

W MOTOR PROTEIN; Microtubulles; Dynein; Flagella; Repeat; WD 2.

FT REPEAT 429 472 WD 2.

FT REPEAT 429 472 WD 3.

FT REPEAT 533 WD 3.

FT REPEAT 537 S77 WD 4.

FT REPEAT 580 620 WD 5.

PREPEAT 580 620 WD 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D38538; BAA07539.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00320; WD40; 4.
                                                                                              101 EKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLSNV--EQCLEHEAVDPKVISIANRVA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE DYNEIN INTERMEDIATE CHAIN FAMILY.
SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS (ALPHA AND BETA), THREE INTERMEDIATE CHAINS AND SEVERAL LIGHT CHAINS.
EIVYSWPPPQATQAGGFKSKEIF--VTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELL 216
                                                 EKRDEESTPAPAEAKSDQKLTNQFNFSERASQTYNNPYRERGTQTE----
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit institutions as long
                                                                                                                                              Conservative
                                                                                                                                                                  25,6%;
                                                                                                                                              21;
                                                                                                                                                                  Score
Pred.
                                                                                                                                              Mismatches
                                                                                                                                                                    No.
                                                                                                                                                                    DB 1;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as its content
                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                        Length 702;
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ϋ́α
                                                                                                                                                                                                                                                                                                                                                                                                                                 WD repeat.
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                                                                                                                                              26;
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                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; Nuclear protein.
DNA_BIND 1246 1381 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00136; DNA_pol_B; 1.
Pfam; PF03104; DNA_pol_B_exo; 1.
PRINTS; PR00106; DNAPOLB.
SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J03268; AAA34888.1; -. EMBL; Z50161; CAA90524.1; -. EMBL; Z71378; CAA55978.1; -. EMBL; Z12126; CAA78111.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + {DNA}{N}.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- SUBCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLY.

ALPHA, BETA, CAMMA, DELTA, AND EPSILON WHICH ARE RES

DIFFERENT REACTIONS OF DNA SYNTHESIS.

-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saiz J.E., Buitrago M.J., Soler A., del Rey F., Revuelta J.L.; "The sequence of a 21.3 kb DNA fragment from the left arm of y chromosome XIV reveals LEU4, MET4, POL1, RAS2, and six new opereading frames.";
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A30211; A30211.
SGD; S0005046; POL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae.",
Mol. Microbiol. 7:215-228(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93188702; PubMed=8446029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00116; DNA_POLYMERASE_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMASE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast
   241
                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPLICATIVE POLYMERASE
PVVATKRONVLODTLLA 257
                             PLVDTSIQGFPQDGLMA 250
                                                               VNGNDESSHDAGISKKVKIDPDSSTDKYLETESSPLKLQSRKLRYANDVQDLLDDV-ENS
                                                                                              IFVTEGLSFQ--LQGHVPVASSSKKDEEEQILAKIVEL----LKYSGDQLERKDTAFIPI
                                                                                                                             KKSQKKSIPIDNFDDILGEFESGEVEKPNILLPSKLRENLNSSPTSE-----FKSSIKR 181
                                                                                                                                                              SHSQQWSRCLSNVEQCL---EHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKS--KE 179
                                                                                                                                                                                              EDWREVD----NSSSDEDTGNLASKDSKRKK--NIKREKDHQITDMLRTQHSKSTLLAHA 127
                                                                                                                                                                                                                             ESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12:403-409(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002064; DNA_pol_B.
                                                                                                                                                                                                                                                                                                                                                                493
759
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7:215-228(1993)
                                                                                                                                                                                                                                                                                                                                                              493
760
                                                                                                                                                                                                                                                                             6.5%;
                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

10 S -> R (IN TEMPERATURE SENSITIVE MUTANT).

10 MI -> IV (IN REF. 1).

106808 MW; 50C9032DE995B5AE CRC64;
                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                             Score 85; DE
Pred. No. 27;
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIVE DNA POLYMERASES: WHICH ARE RESPONSIBLE
                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                             Length 1468;
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RP OCC
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SYV2_HUMAN
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RRPL_TSWV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                       SYV2_HUMAN STANLARL,

SYV2_HUMAN STANLARL,

P26640; Q9UQM2;

01-AUG-1992 (Rel. 23, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

01-MAR-2002 (Rel. 41, Cast annotation update)

16-Yell 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRPL_TSWV1
P28976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JQ135; RRVUTW.

Transferase; Nucleotidyltransferase; RNA-directed RNA postrontence 2875 AA; 331498 MW; 574B3B55CF07C6FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Tomato spotted wilt virus L RNA encodes a putative RNA polymerase."; J. Gen. Virol. 72:2207-2216(1991).
                                                                                                                                                                                                                                                                                                                      1933 SA 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1760 NENALN---KMSSYKDFSKLYPNLKKNEDLYKSTKNLKIDEDAVLE----EDELYKKIAS 1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=91374019; PubMed=1895058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tomato spotted wilt virus (strain Brazilian Br-01) (TSWV).
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tosp
                               NCBI_TaxID=9606
                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D10066; BAA00955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peters D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de Haan P., Kormelink R., de Oliveira Resende R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=36413;
                                                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136
                                                                                                                                                                                                                                                                                                                                                                                                                             188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {RNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                        SKARTFVNISSTVKMTYEENMEKKILEMLKFDLDSYCSFKTCVNLVIKDVNFSMLIPILD 1932
                                                                                                                                                                                                                                                                                                                                                                                                                          FQLQGHVPVASSSKKDEEEQILAKIVELLKYSGD------QLERKDTAF-IPIPLVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEKAINLGKKKSSWKAFF----GVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLEMESVHDIMIKNPETILIAPLNDRDFLLSQLFMYTSPSKRNQLSNQSTEKLALDRVLR 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVEQCLEHEAV--DPKVISIAN-----RVAEIVYSWPPPQATQAGGFKSKEIFVTEGLS 187
                                                                                                     OR G7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldbach R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                   Primates;
                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 84.5;
Pred. No. 71;
                                                   Catarrhini; Hominidae;
                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van Poelwijk F.,
                                                                                                                                        (VALRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
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SEQUENCE FROM N.A

MEDLINE=91378943; PubMed=1898367;

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ETT TTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004046; GST_C.
InterPro; IPR004045; GST_N.
InterPro; IPR002300; tRNA-synt_1a.
InterPro; IPR002300; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val.
Pfam; PF00043; GST_C; 1.
Pfam; PF00043; GST_C; 1.
Pfam; PF00133; tRNA-synt_1; 1.
PFAM; PF00133; tRNA-synt_1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted [5]
                                                                                                                                                                                                                                                                EMBL; AF134726; AAD21819.1; -.
EMBL; AP000503; BAB63303.1; -.
EMBL; M98326; AAAB1332.1; -.
PIR; S17675; S17675.
HISSP, P96142; 1GAX.
                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shiina S., Tamiya G., Oka A., Inoko H.; "Homo sapiens 2,229,817bp genomic DNA of Submitted (SEP-1999) to the EMBL/GenBank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Evidence that gene G7a in the encodes valyl-tRNA synthetase." Biochem. J. 278:809-816(1991).
                                                                     SITE
                                                                                 Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>'</del>-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         valy1-tRNA synthetase.";
Gene 123:181-186(1993).
-i- CATALTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93154582; PubMed-8428657; Vilalta A., Donovan D., Wood L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 201-1263 FROM N.A. MEDLINE-93154582; PubMed-8428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence of the human major histocompatibility complex class III region.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rowen L., Madan A., Qin S., Shaffer T., James
Abbasi N., Dickhoff R., Loretz C., Madan A., I
Lasky S., Hood L.;
                                          BINDING
                                                         SITE
                                                                                                        Aminoacyl-tRNA synthetase;
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                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY. SIMILARITY: THE N-TERMINAL DOMAIN IS SIMILAR TO ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + L-valyl-trna(Val).
ENZYME REGULATION: CAN BE REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR 1-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: FORMS HIGH-MOLECULAR-MASS
                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                     X59303; CAA41990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -L., Campbell R.D.;
J. 281:879-879(1992).
                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing and expression
  344
862
865
51
331
590
    7200
354
864
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51
331
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                                                                                                          Protein biosynthesis; Ligase;
"KMSKS" REGION.
ATP (BY SIMILARITY).
P -> S (IN REF. 1).
A -> G (IN REF. 5).
V -> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enomic DNA of 6p21.3 HLA class EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                     "HIGH"
                                                                                EF-1-GAMMA LIKE.
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                                                                     REGION.
                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGREGATES
                                                                                                                                                                                                                                                                                                                                                                                                               There are no
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                                                                                                          ATP-binding
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                                                                                                                                                                                                                                                                                                                                                                                                      is in
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -

This

between

"A nuclear pore complex protein that contains zinc finger motifs, binds DNA, and faces the nucleoplasm.";

Cell 72:29-38(1993).

-i- FUNCTION: POSSIBLE DNA-BINDING SUBUNIT OF THE NUCLEAR PORE COMPLEX (NPC). THE REPEAT-CONTAINING DOMAIN MAY BE INVOLVED IN ANCHORING COMPONENTS OF THE PORE COMPLEX TO THE PORE MEMBRANE.

H

SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. LOCATED TO THE TERMINAL RING STRUCTURE OF THE NUCLEOPLASMIC CAGE.

DOMAIN: CONTAINS X-F-X-F-G REPEATS.

PTM: PHOSPHORYLATED IN INTERPHASE, HYPERPHOSPHORYLATED DURING MITOSIS. MAY PLAY A ROLE IN THE REVERSIBLE DISASSEMBLY OF THE NUCLEAR PORE COMPLEX DURING MITOSIS.

SINILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST NUP1, NSP1, POM 121 AND MAMMALIAN P62.

SIMILARITY: CONTAINS 4 RANBP2-TYPE ZINC FINGERS.

SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN=BUFFALO; TISSUE=Liver; MEDLINE=93137325; PubMed=8422679;

Sukegawa J., Blobel G.;

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi; ; Murinae; Rat

Rattus

602-613;

622-645

AND 971-993

Rattus norvegicus (Rat).

NCBI\_TaxID=10116;

nucleoporin).

NUP153

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В
Qγ
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Best Local S
Matches 49
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               N153_RAT
P49791;
                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nuclear pore complex protein Nup153 (Nucleoporin Nup153) (153 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GHVPVASSSKKDEEEQILAKIVELLKYSGD----QLERKDTAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLNSAISDIE---VDKKELT----GRTLLSVP-----GYKEKVEFGVLVSFAYKVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRWHRMRGETTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLG----REAFLQEVWKWK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSQSSEKAINLGKKKSS--W-KAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSR 132
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49; Conser
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22.1%;
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RPGKRC (IN REF. 1).
S -> F (IN REF. 5).
M -> I (IN REF. 5).
MISSING (IN REF. 5).
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Pred.
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33;
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DR InterPro; IPR001876; Znf-RanBP.

DR Pfam; PF00641; zf-RanBP; 4.

DR SMART; SM00547; ZnF_RBZ; 4

DR PROSITE; PS01358; ZF_RANBP2_1; 4.

DR PROSITE; PS0199; ZrF_RANBP2_2; 4

DR Nuclear protein; Transport; Repeat; Zinc-finger; DNA-binding; KW Phosphorylation.

4 15

DOWAIN 42 44

POWAIN 42 446

POLY-GLY.

TO DOMAIN 42 446

POLY-GLY.

TO LEING 657 687

RANBP2-TYPE 1.

TALFING 789 818

RANBP2-TYPE 2.

TALFING 789 818

RANBP2-TYPE 4.

SEQUENCE 1468 AA; 152823 MW; C3DFD9697C556A7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.3%; Score 82.5; DB 1; Length 1468; Sest Local Similarity 23.3%; Pred. No. 45; Natches 54; Conservative 36; Mismatches 103; Indels 39;
                                                                                                                                                                                            394 LRKTNORIDKKNSTYDEKNISRONREQESGFSYPNFSIPAANGLSSG---VGGGGGKMRR 450
                                                                                                                                                192 GHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKDTAFIPIPLVDTSIQGF 243
                                                                                                                                                                                                                       132 RCLSNVEQCLEHEAVDPKVISIANRVABIVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQ 191
                                                                                                                                                                                                                                                                                334 SSPLNSPLDRSGIDSTVFQAKKEKVDSQYPPVQRLMTPKPVSIATNRTVYFKPSLTPSGD 393
                                                                                                           451 ERTTHEVASKPSEEEEV---EVPLLPQ-----ISLPISSSSLPTF 487
                                                                                                                                                                                                                                                                                                                                                                       275 RONKVRSTP-YQAPVRROMKAKQLNAQSYGVTSSTARRILQSLEKMSSPLADAKRIPSAV 333
                                                                                                                                                                                                                                                                                                            85 N-----LGKKKSSWKAFFGVVEKEDSQ------STPAKVSAQGQRTLEYQDSHSQOWS 131
                                                                                                                                                                                                                                                                                                                                                                                                            32 RHHVFKSTPALFSP--KLLRTRSLSQRGLGNCSAN-----ESWTEVSWPCRNSQSSEKAI 84
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: June 19, 2002, 16:33:40 ; Search time 31.42 Seconds (without alignments) 770.672 Million cell updates/sec

Perfect score: US-09-771-961-4 1316

MCSTSGCDLEEIPLDDDDLN.....IPLVDTSIQGFPQDGLMACI 252

Scoring table: BLOSUM62 Gapop 10.0 ,

Gapext 0.5

283138 segs, 96089334 residues

rched:

Stal number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database PIR\_71:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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138127	T20978	T20971	A44345	A49651	G82499	T00530	S17675	F83264	F86677	н90576	T13168	AD0663	T14437	RRVUTW	S58250	T00587	T47311	S75831	A84647	A23595	T40340	A35667	A49393	G72346	S63143	T00790	T37702	в23595	10		
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80	80	80	80	80	80.5	80.5	80.5	80.5	81	81	81	81.5	81.5	81.5	82	
6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.2	6.2	
1075	690	496	427	178	1722	1653	851	333	1647	890	715	663	583	372	1123	
Ν	Ν	N	N	N	ш	Ν	2	N	N	N	Ν	N	N	N	N	
в96508	E84945	G64527	T26103	S29886	178879	A36349	AG2469	T23324	T49412	G64740	D85087	T49685	T16007	G96818	A72311	
hypothetical prote	glycinetRNA liga	hypothetical prote	hypothetical prote	ribosomal protein	retinoblastoma bin		hypothetical prote	hypothetical prote	hypothetical prote	[protein-PII] urid	hypothetical prote	RNA polymerase II	hypothetical prote	F9K20.3 [imported]	conserved hypothet	

## ALIGNMENTS

DNA nucleotidylexotransferase (EC 2.7.7.31) - mouse

B23595

N;Alternate names: terminal addition enzyme; terminal deoxyribonucleotidyltransferase C;Species: Mus musculus (house mouse) C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 18-Jun-1999 C;Accession: B23595; S3025 C;Accession: B23595; S3025 R;Koiwai, O; Yokota, T; Kageyama, T.; Hirose, T.; Yoshida, S.; Arai, K.

R;Koiwai, O.; Yokota, T.; Kageyama, T.; Hirose, T.; Yoshida, S.; Arai, K. Nucleic Acids Res. 14, 5777-5792, 1986
A;Title: Isolation and characterization of bovine and mouse terminal deoxynucleotidyl

A;Reference number: A93633; MUID:86286588 A;Accession: B23595

A; Molecule type: mRNA A; Residues: 1-529 <KOI>

A;Cross-references: GB:X04123; NID:g54765; PIDN:CAA27735.1; PID:g54766 R;Doyen, N.; d'Andon, M.F.; Bentolila, L.A.; Nguyen, Q.T.; Rougeon, F. Nucleic Acids Res. 21, 1187-1121, 1993 A;Title: Differential splicing in mouse thymus generates two forms of terminal deoxyn A;Reference number: S30235; MUID:93219079

A; Accession: S30235

A; Status: translation not shown

A;Molecule type: mRNA
A;Residues: 1-25,'M',27-98,'F',100-192,'R',194-286,'Q',288-308,'E',310-366,'D',368-44
A;Residues: 1-25,'M',27-98,'F',100-192,'R',194-286,'Q',288-308,'E',310-366,'D',368-44
A;Cross-references: EMBL:X68670; NID:9287808; PIDN:CAA48634.1; PID:9287809
C;Superfamily: DNA nucleotidylexotransferase
C;Keywords: alternative splicing; magnesium; nucleotidyltransferase; nucleus

Matches Query Match Best Local Local Similarity nes 54; Conserv 8 DLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANESW 67 Conservative 7.6%; 23.5%; 40; Score 99.5; DB Pred. No. 0.81; 0; Mismatches DB 2; 93, Length 529; Indels 43; Gaps 11;

В Ş В δÃ 170 DALDILAENDELRENEGSCLAFMGASSVLKSLPFPI-----TSMKDTEGI-PCLGDKVK 222 223 SIIEGIIEDGESSEAKAVLNDERYKSFKLFTSVFGVGLK----TAEKWFRMGFRTLSKI 277 68 TEVSWPCRNSQSSE-KAINLGKKKSSWKAF---FGVVEKEDSQSTPAKVSAQGQRTL-EY 122

DЬ ğ 123 QDSHSQQWSRC-----LSNVEQCLEHEAVDPKVISIANRVAEIVYSW-PPPQATQAGG 174 QSDKSLRFTKMQKAGFLYYEDLVSCVNR----PEAQAVSMLVKEAVVTFLPDALVTMTGG

Š 175 FKSKEIFVTEGLSFQLQGH----VPVASSSKKDEEEQILAKIVELLKYSG 220

334 -KMTGHDVDFLITSPEATEDEEQQLLHKVTHFWKQQG

hypothetical protein SPAC15A10.02 - fission yeast (Schizosaccharomyces pombe)

```
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; KoO, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T00790; D84/3/
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R;Rounsley, S.D.; Lin, X.; Ketchum, February 1998
submitted to the EMBL Data Library, February 1998
submitted to the EMBL Data Library chromosome II BAC F24L7 genore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37702
R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1997
                                                                                                    A; Map position: 2
A; Introns: 416/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence A; Reference number: Z14204
A; Accession: T00790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                             A;Cross-references: GB:AE002093;
                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1083 <STO>
                                                                                                                                                                                                                                                                                                               A;Reference number: A84420; MUID:20083487
A;Accession: D84737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ubiquitin-specific proteinase homolog F24L7.8 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001 C;Accession: T00790; D84737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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A;Gene: SPDB:SPAC15A10.02
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-450 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z97208; PIDN:CAB10099.1; GSPDB:GN00066; SPDB:SPAC15A10.02
A;Experimental source: strain 972h-; cosmid c15A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z21738
A; Accession: T37702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tatus: translated from GB/EMBL/DDBJ
lecule type: DNA
lesidues: 1-1083 <ROU>
Cross-references: EMBL:AC003974; NID:g2914688; PID:g2914695
                           Query Match
                                                                                                                                                             Gene:
                                                                                                                                                                                  Genetics
                                                                                                                                                                                                                                                                                         Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 RSLSQRGLGN---CSANESWTEVSWPCRNSQSSEKAI----NLGKKKSSWKAFFGVVEKE 103
                                                                                                                                                          At2g32780; F24L7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPFSVPPSRATLTGGYASGSIGLSTPGLSRAPHYELDNGNRLLSKRKLHDLLQQIDSEEK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSSVPETPVGVSAANVSNESTELATSATQQ-SGLANNVEKSQTPSYMSANHLPKVDSKSP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSQ--STPAKVSAQ--GQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSIQQ--LQNRQASSANGNNTGTSTPVNASTDTRKSTASTPQLQQTQAQANAPQQRINPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILAKIVELLKYSGDQLERKDTAF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVYSWPPPQATQAGGFKSKEI-FVTEGLS----FQLQGHVPVASSSKK------DEEEQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEPEVEELLLEIADEFVESVTNF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
57; Conserv
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7.2%;
21.8%;
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                                                                                                                                                                                                           NID: g2914695; PIDN: AAC04485.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 97; DB Pred. No. 1.1;
  Score
Pred.
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95;
No.
DB
5.3;
                        2
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                        Length 1083;
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Вþ Ş В δÃ В Qy

64

131 DEDNVKIDEDNIENELQF-----

8 DLEEIPLDDDDL-NTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGL---GNCSA 63

TPKIKEASILRSSLLGQRNVLNTRNPKS 176

Matches

Conservative

43;

Query Match Best Local Similarity

6.8%; 21.4%;

Score 90; Pred. No. Mismatches

DB 2; Length 433 107;

Indels

52;

Gaps

10;

В δÃ

162 YSW-----PPPQATQAGGF-----KSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQIL 209

LQKKRELIESKWHRLLFHDKKMVEKKLESLREYERKRMPPRGTDVSSSEQDNSFKISTPT 296

----QDSHSQQWSRCLSN----VEQCL-----EHEAVDPKVISIAN------RVAEIV 161

KESHIKVKPIINNKSSSQRKSSAALRKQLGKPLPLPYLNSPNSDSTPTLQRKEEVFTDEV 236 NESWTEVSWPCRNSQSSEKAINLGKKKSSWKAF-FGVVEKEDSQSTPAKVSAQGQRTLEY 122

KSYVSLEQKPLPNLSAMNNFNDVTDNKEKEETNNNILKFQAQRDPLQILQSEIEMHTKKL

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A;Cross-references: EMBL:Z71464; NID:gl302176; PIDN:CAA96082.1; PID:e239561; PID:gl30 A;Experimental source: strain S288C R;Rose, M.D.; Fink, G.R. Cell 48, 1047-1060, 188. Cell 48, 1047-1060, 189. A;Title: KAR1, a gene required for function of both intranuclear and extranuclear mic A;Reference number: A26455; MUID:87159524 A;Accession: A26455
A;Map position: 14L
C;Keywords: transmembrane protein
F;413-429/Domain: transmembrane #status predicted
                                                                               A;Gene: SGD:KAR1
A;Cross-references: SGD:S0005132; MIPS:YNL188w
                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-198,'V',200-433 <ROS>
A;Coss-references: GB:M15683; NID:g171776; PIDN:AAA34716.1; PID:g171777
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Obermaier, B.; Piravandi, E.; Rinke, M.; submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 29-Oct-1999
C;Accession: S63143; A26455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QУ
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                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-433 <OBE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S63143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell division control protein KAR1 - yeast (Saccharomyces cerevisiae) N; Alternate names: protein N1611; protein YNL188\omega
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 --- ASSSKKDEEEQILAKIVELL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 NRVA--EIVYSWPPPQAT------QAGGFKSKEIFVTEGLSFQLQGHVPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           903 EENTKQAPITSVTETPLLGGETISSQPASDNECENW------EDLAVDSEEV-IV 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                846 NRWVNENGASSAFDECRDSSLNQSCIDL---ENGYKAAPPITKLPNCKEEESAIDDGFVG 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      786 DSDPAVLDESDSPVSVDRCLAQFTKHEILSEDNAWHCENCSKNLKLQRLREKRRTKEGLS 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEDSQSTP----AKVSAQGQRTLEYQ---DSHSQQWSRCLSNVEQCLEHEAVDPKVISIA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCSANESWTEVSW-PCRNSQSSEKAINLGKKKSSWKAF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domdey, ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FSPKLLRTRSLSQRGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
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activator 1 large chain - mouse
N;Alternate names: replication factor 1 large chain
C;Species: Mus musculus (house mouse)
C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change
C;Accession: A49393; A56200; A56284; JC4226
R;Burbelo, P.D.; Utani, A.; Pan, Z.O.; Yamada, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 11543-11547, 1993
A;Title: Cloning of the large subunit of activator 1 (replicatic
                                           A; Molecule type: mRNA
A; Residues: 1-1131 < SUR>
A; Residues: 1-1131 < SUR>
A; Cross-references: GB:U01222; NID:g405111; PIDN:AAA21643.1; PID:g405112
R; Luckow, B.; Bunz, F.; Stillman, B.; Lichter, P.; Schuetz, G.
Mol. Cell. Biol. 14, 1626-1634, 1994
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C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: G72346
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A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-647 <ARN>
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                A; Title: Cloning, expression,
                                                                                                                                                                                                                             A; Reference number: A49393; MUID: 94089669 A; Accession: A49393
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A;Reference number: A72200; MUID:99287316
Accession: G72346
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                                                                                                                                                                                                A; Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 ETRSL-----PQNSDAAKL-SRDFEKTTGIKNEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 RTHDISTEKLLTSTEHEEKKENGFLVKDSENKESASQISFEKKHSS----IPYLESETSR 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---TGNEIKMSKLSFVPLLPADEKQQSSNGDG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVAEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVEL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SESNKKLSSSFRTPAEPSLKSESTKVFKE-----QPISAQDKETKHSARQP----IFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-----TPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIAN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTRSLSQRGLGNCSANESWTEVSWPCRNSQSSEKA--INLGKKKSSWKAFFGVVEKEDSQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSSKLIKEIKTTDDKSSEKHVLEEVSKRDENHAEYR----KSEQGIFKS------ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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     A56200; MUID:94158835
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21.3%; Pred. No. 8
                                   and chromosomal localization of the 140-kilodalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DLNTIEFKILAYYTRHHVFKSTPALFSPKLL 48
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son, D.;
                                                                                                                                                                                                                                               Ty transcription activator TEC1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YBR0750; protein YBR083w C;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: A35667; S45950
                                                                                                         R;Laloux, I.; Dubois, E.; Dewerchin, M.; Jacobs, E. Rol. Cell. Biol. 10, 3541-3550, 1990 A;Title: TECl, a gene involved in the activation of A;Reference number: A35667; MUID:90287143 A;Accession: A35667
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A;Cross-references: GB:M32797; NID:g172881; PIDN:AAA35141.1; PID:g172882 R;Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; V
                                                    A; Molecule type: DNA
A; Residues: 1-486 <LAL>
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A; Molecule type: mRNĀ A; Molecule type: mRNĀ A; Residues: I-65, N',67-613,615-944, 'S',946-1070, 'A',1072-1131 <MCG> A; Residues: I-65, N',67-613,615-944, 'S',946-1070, 'A',1072-1131 <MCG> A; Cross-references: GB:U36441; NID:g1022775; PIDN:AAA79698.1; PID:g1022776 R; Halligan, B.D.; Teng, M.; Guilliams, T.G.; Nauert, J.B.; Halligan, N.L.N. Gene 161, 217-222, 195
A; Title: Cloning of the murine cDNA encoding VDJP, a protein homologous to the A; Reference number: JC4236; MUID:95394359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'MVEN', 63-486 <HAL>
A; Residues: 'MVEN', 63-486 <HAL>
A; Cross-references: GB: M88489; NID: g1066814; PIDN: AAA81558.1; PID: g1066815
A; Experimental source: A20 lymphoid cell line
C; Comment: This protein binds to the nonamer portion of the variable, diversignal sequence-dependent fashion.
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A; Residues: 1-944, 'S', 946-1131 < LUC>
A; Cross-references: GB: X72711; NID: g457741; PIDN: CAA51260.1; PID: g457742
A; Cross-references: GB: X72711; NID: g457741; PIDN: CAA51260.1; PID: g457742
R; MCGehee Jr., R.E.; Habener, J.F.
MOL. Endocrinol. 9, 487-501, 1995
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A;Reference number: A56284; MUID:95388065
A;Accession: A56284
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A; Status: preliminary
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Best Local Similarity
686 FYTSG 690
                                                                   243 FPQDG 247
                                                                                                                                                                                                                                                                                                   577 ASLKNIIGQQGDQSCANKLLRWLRNWHKSSPEEKKHAAKFGKLASKD----DGSSFKAAL 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                       521 ESESKKCKLTLLKNSPMKAVKKEASTCPRGLDVKETHGNR----SSNKEECLLWVDKYKP 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 LGTKILDEDGLLDLIRTMPGKRSKYEMAAEAEMKKEKSKLERTPQKNDQGKRK-ISPAKK 520
                                                                                                                                                                                                                           190 LQGHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKDT-----AFIPIPLVDTSIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 KSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCL----EHEA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 LRTRSLSQRGL------GNCSANESWTEVSW-----PCRNSQSSEKAINLGKK 89
                                                                                                                                                   LSGPPGVGKTT-----TASLVCQELGYSYVELNASDTRSKNSLKAVVAESLNNTSIKG
                                                                                                                                                                                                                                                                                                                                                                               VDPKVI-----SIANRVAEIVYSW-----PPPQATQAGGFKSKEIFVTEGLSFQ--- 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7%; Score 88.5;
23.7%; Pred. No. 21;
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C;Superfamily: Ty transcription activator TEC1; TEA DNA-binding
C;Keywords: DNA binding; nucleus; transcription regulation
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submitted to the EMBL Data Library, March 1997
A; Reference number 221922
ccession: T40340
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A; Residues: 1-486 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SPBC3B9.01 - fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Schizosaccharomyces pombe;Date: 03-Dec-1999 #text_change 03-Dec-1999;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-287 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: T40340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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123 QDSHSQQWSRCLSNVEQCLEHEAVDPKVISI--ANRVAEIVYSWPPPQATQAGGFKSKEI 180
                                                                                   109 IATAVQNNPKSQQAL---IENDGLKILFGALKKEDSDETKNKVLYAITSELKLNEAGIAL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 LLTPITASNEKKIENFI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 GHVPVASSSKKDEEEQI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 LLHLIEHGAEQTTENSNLFYDIFEEIIDSL--PSVSDSGSLTPKNLYVSNNSSGLSVHSK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 VISIANRVA-----EIVYSWPPPQATQAGGFKSKEIFV---TEGLSFQLQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 KIRNANFG---RNELISLYIKHKTNEFRTKKQISSHIQVWKKTIQNKIKDSLTLSSKEKE 212
                                                                                                                                                                                                                                                           56 VPLDQKE---IAFDNLEMLVEHIDNANNLVPLQLWPRLLKQLESPESTLRRLAA---WT- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                                                                                          12 IPLDDDDLNTIEFKILAYYTRH--HVFKSTPALFSPKLLRTRSLSQRGLGNCSANESWTE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 ----AFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLSN-VEQCLEHEAVDPK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 QRKNEVPNISVSNYFPGQSSETSSTTE-SWTIGCDKWSEKVEEAFLEALRLIMKNGTTKI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 LLRTR----SLSQRGLGNCSANESWTEVSWPCRNSQSSEK-----AINLGKKKSSWK- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPDB: SPBC3B9.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STSGCDLEEIPLDDDDLNTIEFKILAYYTRHHVFK------STPALFSPK 46
                                                                                                                                                                       VSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKV-----SAQGQRTLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:AL022070; PIDN:CAA17781.1; GSPDB:GN00067; SPDB:SPBC3B9.01
                                                                                                                                                                                                                                                                                                                                                                                                                      6.6%; Score 87.5; DB 2; 21.2%; Pred. No. 4.1; tive 41; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
22.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skelton, J.; Churcher, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Length 486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Rocessaude type: protein
A; Molecule type: protein
A; Rosidues: 221-226, 'X', 228-231, 'X', 235-249 <PA2>
A; Residues: 221-226, 'X', 236-249, 'X', 236-2
                                       Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A;Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible
A;Reference number: I45884; MUID:87213162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Alternative splicing of bovine tA; Reference number: PC2127; MUID:94264411 A; Accession: PC2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Pandey, V.N.; Modak, M.J.
J. Biol. Chem. 264, 867-871, 1989
A;Title: Biochemistry of terminal deoxynucleotidyltransferase.
A;Reference number: A32198; MUID:89093157
A;Accession: A32198
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J. Biol. Chem. 263, 3744-3751, 1988
A;Title: Biochemistry of terminal deoxynucleotidyltransferase.
A;Reference number: A29948; MUID:88153669
A;Accession: A29948
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A;Residues: 143-179,"x,181-187,"xxxxxx",194-199,"xx",202-230,"xxx",234-303;322-363,
A;Residues: Chardy L.C.; Mattaliano, R.J.; Chang, L.M.S.; Bollum, F.J.
Proc. Natl. Acad. Sci. U.S.A. 81, 4363-4367, 1984
A;Title: Molecular cloning of human terminal deoxynucleotidyltransferase.
A;Reference number: A93995; MUID:84272638
A;Accession: A05052
                                                                                                                                                          A;Cross-references: GB:D17452
R;Koiwai, O.; Kaneda, T.; Morishita,
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 511-519 <TA2>
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 303-320 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 221-226, 'X',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 335-348,'X',350-355;366-377,'XX',380-381,'X',383-386;521-526,'X',528-533,
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                                                                                                                                                                                                                                                                                                                                      A; Accession: PC2128
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228-231, 'X', 235-249

T.; Hashimoto, Y.;

Noda, A

transferase

Identification

and uni

Affinity labeling

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Db	
QУ	181 FVTEGLSFQLQGHVPVASSSKKDEEEQILAKIVELLKYSGDQLERKDTAFIPIPLVDTSI 240
Db	209 ILQKAHEFQIPEKVYQFSLEHSVDEDCVTKSLHTLYLFQKKKVSVANTNELLKSLVQFKS 268
Qy	241 QGFPQ 245
Db	269 E-FPE 272
RESULT	
A23595 DNA nu N;Alte	A23595 DNA nucleotidylexotransferase (EC 2.7.7.31) long form – bovine N;Alternate names: terminal addition enzyme; terminal deoxyribonucleotidyltransferase
C;Sp C;Da	<pre>C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999</pre>
C; Ac	C;Accession: A23595; A60467; A05052; A29948; A32198; PC2127; PC2128; I45884 R;Koiwai, O.; Yokota, T.; Kaqeyama, T.; Hirose, T.; Yoshida, S.; Arai, K.
Nucl	Nucleic Acids Res. 14, 5777-5792, 1986
A;Ti A;Re	Itle: Isolation and characterization of bovine and mouse terminal deference number: A93633; MUID:86286588
A; Ac	A;Accession: A23595
A;Mo	A; Molecule type: mRNA A: Residues: 1-302 321-510 520-547 CKOTS
A;Cr	A;Cross-references: GB:X04122; NID:g767; PIDN:CAA27734.1; PID:g768
A; No	A; Note: it is uncertain whether Met-1 or Met-12 is the initiator
R; EV	R;Evans, R.K.; Beach, C.M.; Coleman, M.S.
7 . 7 . (	7-14-1-0

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C;Genetics:
A;Gene: At2g25320
A;Map position: 2
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-13 <KO2>
A; Cross-references: GB:M26146; NID:g951177; PIDN:AAA87354.1; PID:g951178
C; Comment: This protein can be isolated as a single polypeptide chain or as a heterodime C; Genetics:
A; Gene: DNTT
C; Superfamily: DNA nucleotidylexotransferase
C; Keywords: alternative splicing; magnesium; nucleotidyltransferase
C; Keywords: alternative splicing; magnesium; nucleotidyltransferase
F;1-510,520-547/Product: DNA nucleotidylexotransferase long form II #status predicted <MP
F;1-302,321-547/Product: DNA nucleotidylexotransferase short form #status predicted <MP
F;1-302,321-547/Product: DNA nucleotidylexotransferase short form #status predicted <MP
F;1-307,7Region: substrate binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2g25320 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C:Accession: A84647
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A;Molecule type: DNA
A;Residues: 1-1660 <STO>
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A;Accession: A84647
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   RGAIVA--QAVAMVLEKQRVQS-PNLNATSGDASLKHQDPVLEGEASEQPATGGTEFRII 1249
                                                                          LGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQD-----SHSQQWS-----RCL 134
                                                                                                                                                    MADLMEEHIFYANRQFFDVYILLEMLSIS-----CLAEEA------SQTFERAVA 1192
                                                                                                                                                                                                                           LAYYTRHHVFKSTPALFSPK-LLRTRSLSQRGLGNCSANESWTEVSWPCRNSQSSEKAIN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VESTFEKFKLPSRQVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGFRRGKKI------GHDVDFLITSPGSAEDEEQLLPKVINLWEKKGLLLYYDL 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSW-PPPQATQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WFRMGFRSLSKIMSDKTLKFTKMQKAGELSLLKIPIIAMGWSG-FGFLYYEDLVSCVTRA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WTEVSWPCRNSQSSEKAINLGKKKSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIIEEI---IEDGESSEVKAVLNDERYQSFKLFTSVF------GVG-LKTSEK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDLEEIPLDDDDLNTIEFKILAYYTRHHVFKSTPALFSPKLLRTRSLSQRGLGNCSANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                 6.6%;
24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425
                                                                                                                                                                                                                                                                                                         31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87; DB Pred. No. 11; 33; Mismatches
                                                                                                                                                                                                                                                                                                                                         Score 87; DB
Pred. No. 49;
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ι,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VKEAVWAFLPDAFVTM 359
                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WKAFFGVVEKEDSQSTPAKV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81;
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                                                                                                                                                                                                                                                                                                                                                                        Length 1660
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                     58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                         hypothetical protein T32All.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47311
                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-889 <RIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
A; Experimental source: cultivar Columbia; BAC clone T32A11
                                       A; Cross-references: EMBL: AL138653
                                                                                                                                                                                A; Reference number: Z24459
A; Accession: T47311
                                                                                                                                                                                                                                                          submitted to the Protein
                                                                                                                                                                                                                                                                                              R;Rieger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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12

M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; to the Protein Sequence Database, April 2000

Mewes,

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hypothetical protein slr1285 - C;Species: Synechcystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_1 C;Accession: S75831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18290.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-464 < KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S75831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; I
DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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290
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                                                                                                                                                                                                                                                                                                                                       94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                   WTEVS-WPCRNSQSSEKA-----
ELESTPLPELVVPLTVTSLEAVFQAGI 316
                                            -----IPIPLVDTSIQGFPQDGL 248
                                                                                            LLQALTHEVR--TPLTSIRTLTKLLLRRKDLSPEVLKRIESIDRECSDQISRMDLIFRAT 289
                                                                                                                                    VTEGLSFQLQGHVPVAS-----SSKKDEEEQILAKIVELLKYSGDQLERKDTAF---
                                                                                                                                                                                                                                                                                  AQFYWTFDPEILQQAWLSLQARLKYGLSPDLSLLQKTIAAFNFPQPDFRLVTYFGQLMLD
                                                                                                                                                                                                                                                                                                                                    KAFFGVVEKEDSQSTPAKVSAQ----
                                                                                                                                                                                                                                                                                                                                                                                 WEEFSPWPCLAGEESEWSAVPPMREIPLFPQDPLAEEQFCWLMTPQFGLLLLLGKNEQGL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLVDRFTSPTSSSHDLDLELEILAILI 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNLAETLTHSR-DPQVRGFVKMLYTILFKWFPDQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIFVTEGLSFQLQ--- 191
                                                                                                                                                                                                                                   YQDSHSQQWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKSKEIF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                        ---YNLPPCQEQESAEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S74322; MUID:97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 85.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----INLGKKKSSW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E.; Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PFRVQILR 1290
                                                                                                                                                                                                                                                                                                                                  -GORTLE 121
                                                                                                                                                                                        --SPDVE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                     207
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Yamada, M.; Ya
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A; Map position: 3
A; Introns: 88/3; 2
A; Note: T32All.100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                                                                         A;Introns: 111/1; 183/3; 448/3; 738/2; 882/3 C;Superfamily: ubiquitin-activating enzyme E1 C;Keywords: ligase; nucleotide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: Arabidopsis thaliana chromosome A;Reference number: Z14178
A;Accession: T00587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis thaliana N;Alternate names: protein T27E13.15; ubiquitin activating enzyme (UBA1); ubiquitin activation enzyme (UBA1); ubiquitin activatin enzyme (UBA1); ubiquitin activation enzyme (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1080 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: F84704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1080 <ROU>
A;Cross-references: EMBL:AC004165; NID:g3150396; PIDN:AAC16961.1; PID:g3150409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rounsley, S.D.; Lin, X.; Ketchum, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 AVDPKVISIANRVAEIVYSWPPPQATQAGGFKS----KEIFVT-----EGLSFQLQG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 LLDLLLDDSTSKTILHWKRLTHPKQVISLPQIHALESNLKLPVDPLI------VGDL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 NADQSWAEWDDEVKDKKVAYMYDLILASHQFQKTDWPRGDATLPPISFPKKKLSGVHKKH 353
96 FFGVVEKEDSQSTPAKVSAQGQRTLEYQDS----HSQQWSRCLSNVEQCLEHEAVDPKVI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 NLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLSNVEQCLEHE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T27E13.15; At2g30110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANESWTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEIPLDDDDLNTI-EFKILAY-----YTRHHVFKSTPALFSPKLLRTRSLSQRGLGNC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TKVEELSNRVMKL-----EKAKKAVRFKRSTKLSSSFVACSSRSKRKKTMEVPIQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AE002093; NID:g3150409; PIDN:AAC16961.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
                                                                                                                                                                6.5%;
24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5%; Score 85.5;
19.0%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                        Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      May 1998
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                                                                                                                          Mismatches
                                                                                                                                                                                                      DВ
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                                                                                                                                                                                                      2;
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                                                                                                                          54;
                                                                                                                                                                                                  Length 1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T27E13 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                          Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme (UBA1); ubiquitin-act
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                                          A; Gene:
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A; Molecule type: DNA
A; Residues: 1-26 <MOUS
A; Residues: 1-26 <MOUS
A; Cross-references: EMBL:Z12126; NID:g3929; PIDN:CAA78111.1; PID:g3932
R; Saiz, J.E.; Buitrago, M.J.; Soler-Mira, A.; Del Rey, F.; Revuelta, J
submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1468 <SAI>
A;Cross-references: EMBL:Z50161; NID:g929846; PIDN:CAA90524.1; PID:g929851
A;Cross-references: EMBL:Z50161; NID:g929846; PIDN:CAA90524.1; PID:g929851
A;PIC:Z3292111, A; Valsasnini, P.; Flevani, P.; Lucchini, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 3772-3776, 1988
A;Title: DNA polymerase I gene of Saccharomyces cerevisiae: nucleotide sequence, mapp
A;Reference number: A30211; MUID:88234507
A;Accession: A30211
                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1468 <SAF>
A; Cross-references: EMBL: Z50161;
                                                                                                                                                                                                                                                                                           Yeast 12, 403-409, 1996
A;TitLe: The sequence of a 21.3 kb DNA fragment from the left arm of yeast chromosome
A;Reference number: 563948; MUID:96267765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The general amino acid control regulates MET4, which encodes a methionine-pa A;Reference number: S31199; MUID:93188702
A;Accession: S31201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIN:89798, NCBIP:89808) R;Mountain, H.A.; Bystroem, A.S.; Korch, C. Mol. Microbiol. 7, 215-228, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: Luc ucunt R;Thomas, D; Jacquemin, I; Surdin-Kerjau, AMO1. Cell. Biol. 12, 1719-1727, 1992
A;Title: MET4, a leucine zipper protein, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-758, 'IV', 761-1468 < PIZ>
A; Residues: 1-758, 'IV', 761-1468 < PIZ>
A; Cross-references: EMBL:J03268; NID:g172208; PIDN:AAA34888.1; PID:g172209
A; Cross-references: EMBL:J03268; NID:g172208; PIDN:AAA34888.1; PID:g172209
A; Note: the authors translated the codon CAT for residue 653 as Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 13-Jan-1996 #sequence_revision 23-Feb-1996 #text_change 20-Jun-2000 C;Accession: S58250; A30211; C42246; S31201; S63042; S63952; S22774 R;Saiz, J.E.; Buitrago, M.J.; Soler, A.; Herrich Rey, F.; Revuelta, J.L. submitted to the EMBL Data Library, July 1995 A;Description: The sequence of a 21.3 kb fragment from the left arm of yeast chromoso A;Reference number: S58246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S63037
A; Accession: S63042
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A; Residues: 1-6 <THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A42246; A; Accession: C42246
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A; Residues: 1-14
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                                                                    C; Genetics:
                                                                                                     A; Note:
                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Saiz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1468 <SAW>
A;Cross-references: EMBL:Z71378; NID:g1302015; PIDN:CAA95978.1; PID:g1302016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: Z12126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S58250
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                                                                                                                                                                                                                                           A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                  J.E.; Buitrago, M.J.; Soler-Mira, A.; del Rey, F.; Revuelta, 2, 403-409, 1996
                                                                                                     the nucleotide sequence was
                                SGD:POL1; CDC17;
                                                                                                                                                                                                                                                                                   S63952
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SGD:S0005046;
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                                                                                                                                                                                                                                               not shown;
                                                                                                                                         NID:g929846; PIDN:CAA90524.1; PID:g929851
                                                                                                 submitted
                                                                                                                                                                                                                                               translation
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                                                                                                     Library, July 1995
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MIPS:YNL102w

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RRVOTW

RYOTW

genome polyprotein - tomato spotted wilt virus (strain BR-01)

N;Alternate names: L protein

N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)

C;Species: tomato spotted wilt virus

C;Species: tomato spotted wilt virus

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 29-May-1998

C;Accession: J01335

C;Accession: J01335

A;Ge Haan, P.; Kormelink, R.; de Oliveira Resende, R.; van Poelwijk, F.; Peters,

J. Gen. Virol. 71, 2207-2216, 1991

A;Title: Tomato spotted wilt virus L RNA encodes a putative RNA polymerase.

A;Reference number: J01335

A;Residues: 1-2875 < DEH>

A;Residues: 1-2875 < DEH>

A;Residues: 1-2875 < DEH>
Search completed: June 19, 2002, 16:33:44 Job time: 77 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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Best Local Similarity
Thes 51; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Map position: 14L
C:Superfamily: herpesvirus DNA-directed DNA polymerase
C:Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uery Match
Best Local Similarity 22.0
40; Conservative
                                                                                                                                                                                                                      1873 SKARTFVNISSTVKMTYEENMEKKILEMLKFDLDSYCSFKTCVNLVIKDVNFSMLIPILD 1932
                                                                                                                                                                                                                                                                                                                        1813 SLEMESVHDIMIKNPETILIAPLNDRDFLLSQLFMYTSPSKRNQLSNQSTEKLALDRVLR 1872
                                                                                                                                                                                                                                                                                                                                                                                                                            1760 NENALN---KMSSYKDFSKLYPNLKKNEDLYKSTKNLKIDEDAVLE----EDELYKKIAS 1812
                                                                                                                            1933 SA 1934
                                                                                                                                                                                                                                                                    188 FQLQGHVPVASSSKKDEEEQILAKIVELLKYSGD------QLERKDTAF-IPIPLVD 237
                                                                                                                                                                                                                                                                                                                                                                         136 NVEQCLEHEAV--DPKVISIAN-----RVAEIVYSWPPPQATQAGGFKSKEIFVTEGLS 187
                                                                                                                                                                             238 TS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PVVATKRONVLODTLLA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 PLVDTSIQGFPQDGLMA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 VNGNDESSHDAGISKKVKIDPDSSTDKYLEIESSPLKLQSRKLRYANDVQDLLDDV-ENS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 IFVTEGLSFQ--LQGHVPVASSSKKDEEEQILAKIVEL----LKYSGDQLERKDTAFIPI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 KKSQKKSIPIDNFDDILGEFESGEVEKPNILLPSKLRENLNSSPTSE-----FKSSIKR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 SEKAINLGKKKSSWKAFF----GVVEKEDSQSTPAKVSAQGQRTLEYQDSHSQQWSRCLS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 SHSQQWSRCLSNVEQCL---EHEAVDPKVISIANRVAEIVYSWPPPQATQAGGFKS--KE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 EDWREVD----NSSSDEDTGNLASKDSKRKK--NIKREKDHQITDMLRTQHSKSTLLAHA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 ESWTEVSWPCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAQGQRTLEYQD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%; Score 84.5; DB 1; Length 2875; 22.0%; Pred. No. 1.7e+02; 1tive 40; Mismatches 73; Indels 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%; Score 85; DB 2; Length 1468; 25.9%; Pred. No. 62; ative 29; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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